



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 175930**

**TO: Manjunath N Rao**  
**Location: REM-2A01/2C70**  
**Art Unit: 1652**  
**Friday, January 13, 2006**  
**Case Serial Number: 10/618252**

**From: Kristine Hensle**  
**Location: Biotech-Chem Library**  
**REM-1B69**  
**Phone: (571) 272-4161**

**Kristine. Hensle@uspto.gov**

### **Search Notes**

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle  
Librarian  
STIC Biotech/Chem Library  
(571)272-4161

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STIC-Biotech/ChemLib

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From: Rao, Manjunath N.  
Sent: Saturday, January 07, 2006 11:44 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request for 10618252

From: Manjunath N. Rao  
Art Unit 1652, Room 2A01  
Mail Box in Room 2C70  
Phone: 272-0939

Date: 1-7-06

Please search the following as soon as possible for application with serial number  
**10/618252**

1. SEQ ID NO: 14 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results
2. SEQ ID NO: 15 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

If you have any questions please call me at the above phone number.

Thanks

1/9/2006

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:

Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: January 12, 2006, 02:08:14 ; Search time 17761 Seconds  
(without alignments)  
11540.875 Million cell updates/sec

Title: US-10-618-252-14

Perfect score: 3606

Sequence: 1 acgcgtccgcctccatctcgtc.....atttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_scs:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3606	100.0	3606	6	AX009206	AX009206 Sequence
2	3463.8	96.1	7747	9	AY360383	AY360383 Mus muscu
3	3078.8	85.4	3373	9	AF110507	AF110507 Mus muscu
4	3064	85.0	7618	6	AX105862	AX105862 Sequence
5	3050.4	84.6	7581	6	AX105861	AX105861 Sequence
6	2912.4	80.8	3427	6	E60027	E60027 Novel phosp
7	2912.4	80.8	3427	6	AB027155	AB027155 Rattus no
8	2610.6	72.4	3219	6	AX687065	AX687065 Sequence
9	2167	60.1	3080	6	E60028	E60028 Novel phosp
10	2141.6	59.4	3353	9	AY462095	AY462095 Rattus no
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12	2139.4	59.3	3015	9	AY462092	AY462092 Rattus no
13	2139.4	59.3	3030	9	AB027156	AB027156 Rattus no
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## ALIGNMENTS

RESULT 1  
LOCUS AX009206 3606 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 14 from Patent EP0967284.  
ACCESSION AX009206  
VERSION AX009206.1 GI:9996571

KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE  
1 Lanfear, J. and Robas, N.M.  
Phosphodiesterases  
Patent: EP 0967284-A 14 29-DEC-1999;  
PRIZER LTD (GB); PRIZER (US)

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1 ACCCGTCGGCTCTTCAATCTGCTTCCACCTCCCGGCGCTCCCGAGAGGCGC 60  
DB 1 ACCCGTCGGCTCTTCAATCTGCTTCCACCTCCCGGCGCTCCCGAGAGGCGC 60  
QY 61 AGCGGGGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
61 AGCGGGGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
DB 61 AGCGGGGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 121 AGGACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
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QY 181 CAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
181 CAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240

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Qy      ||| 1261 GACATATCTTGTATACATAGTTGCCATAGACTCTGTACTTGAACATCATGATATAT 1320

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 ORGANISM Mus musculus  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Mus.  
 REFERENCE  
 AUTHORS Hebbs, A.L., Robertson, H.A. and Denovan-Wright, E.M.  
 TITLE Striatal phosphodiesterase mRNA and protein levels are reduced in  
 Huntington's disease transgenic mice prior to the onset of motor  
 symptoms  
 JOURNAL Neuroscience 123 (4), 967-981 (2004)  
 PUBMED 14751289  
 REFERENCE  
 AUTHORS Hu, H., McCaw, E.A., Hebbs, A.L., Gomez, G.T. and Denovan-Wright, E.M.  
 TITLE Striatum-specific isoforms of phosphodiesterase 10A  
 JOURNAL Eur. J. Neurosci. 20 (12), 3351-3363 (2004)  
 PUBMED 15610167  
 REFERENCE  
 AUTHORS Hu, H., McCaw, E.A., Hebbs, A.L.O., Gomez, G.T. and Denovan-Wright, E.M.  
 TITLE Direct Substitution  
 JOURNAL Submitted (01-AUG-2003) Department of Pharmacology, Dalhousie  
 University, 5859 University Avenue, Tupper Medical Building, Rm15D,  
 Halifax, NS B3H 4H7, Canada  
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ORIGIN

Query Match 96.1%; Score 3463.8; DB 9; Length 7747;  
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VERSION AF110507.1 GI:4883490  
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SOURCE  
ORGANISM  
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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Soderling, S.H., Bayuga, S.J. and Beavo, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 96 (12), 7071-7076 (1999)  
DIRECT SUBMISSION  
Submitted (02-DEC-1998) Pharmacology, Univ. of Washington, Seattle,  
WA 98195, USA  
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## ORIGIN

Query Match 85.4%; Score 3078.8; DB 9; Length 3373;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3080; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 VERSION AX105862.1 GI:13921870  
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 ORGANISM Mus sp.  
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 AUTHORS Robertson, H.A. and Denovan-Wright, E.M.  
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QY	1965	TTGAA	CTTGA	AAAAATTTG	CCGTTTAT	CA	TGTCATG	ATCTGTGTA	AGAGAA	CA	TATGCGCGGTTTC	2024						
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ACCESSION E60027.1 GI:18630000  
VERSION E60027.1  
KEYWORDS JP 2000224992-A/15.  
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ORGANISM Rattus sp.  
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Sciurognathi; Muridae; Murinae; Rattus.  
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Omorik K., Kodera A., Fujishige K., Michihata H. and Yuasa K.  
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PF 11-MAY-1999 JP 1999129343  
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 REFERENCE  
 1 Fujishige, K., Kotera, J. and Omori, K.  
 Striatum- and testis-specific phosphodiesterase PDE10A isolation  
 and characterization of a rat PDE10A  
 Eur. J. Biochem. 266 (3), 1118-1127 (1999)  
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 Omori, K., Fujishige, K. and Kotera, J.  
 Direct Submission  
 Submitted (12-MAY-1999) Kenji Omori, TANABE Seiyaku Co. Ltd.,  
 Discovery Research Laboratory, 2-50 Kawagishi-2-chome, Toda,  
 Saitama 335-8505, Japan (E-mail: k-omori@toda.co.jp,  
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 REFERENCE  
 1 James, J.C., Lebel, L.A., Menniti, F.S. and Strick, C.A.  
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ACCESSION E60028.1 GI:18630001  
VERSION JP 2000224992-A/16.  
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SOURCE Rattus sp.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 3080)  
Omolı.K., Kodera,A., Fujishige,K., Michihata,H. and Yuasa,K.  
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PD 15-AUG-2000  
PR 11-MAY-1999 JP 1999129343  
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C12N5/10,C12N5/16,  
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 VERSION  
 AY462095.1 GI:42600940  
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 SOURCE  
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 Rattus norvegicus  
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REFERENCE  
 1 (bases 1 to 3353)  
 O'Connor, V., Genin, A., Davis, S., Karishma, K.K., Doyere, V., De  
 Zeeuw, C.I., Sanger, G., Hunt, S.P., Richter-Levin, G., Mallet, J.,  
 Laroche, S., Blise, T.V.P. and French, P.J.  
 Differential Amplification of Intron-containing Transcripts Reveals  
 Long Term Potentiation-associated Up-regulation of Specific Pde10A  
 Phosphodiesterase Splice Variants

TITLE  
 JOURNAL  
 PUBLISHED  
 2 (bases 1 to 3353)  
 French, P.J., O'Connor, V., Genin, A., Davis, S., Karishma, K.K.,  
 Doyere, V., de Zeeuw, C., Sanger, G., Hunt, S.P., Richter-Levin, G.,  
 Mallet, J., Laroche, S. and Blise, T.V.P.  
 Direct Substitution  
 Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre,  
 P.O. Box 1738, Rotterdam 3000DR, The Netherlands

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 AY462091  
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 Rattus norvegicus  
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 1 (bases 1 to 3015)  
 O'Connor, V., Genin, A., Davis, S., Karishma, K.K., Doyere, V., De  
 Zeeuw, C.I., Sanger, G., Hunt, S.P., Richter-Levin, G., Mallet, J.,  
 Laroche, S., Blais, T.V.P. and French, P.J.  
 Differential Amplification of Intron-containing Transcripts Reveals  
 Long Term Potentiation-associated Up-regulation of Specific Pde10A  
 Phosphodiesterase Splice Variants  
 J. Biol. Chem. 279 (16), 15841-15849 (2004)  
 JOURNAL  
 PUBMED 14752115  
 REFERENCE 2 (bases 1 to 3015)  
 AUTHORS French, P.J., O'Connor, V., Genin, A., Davis, S., Karishma, K.K.,  
 Doyere, V., de Zeeuw, C., Sanger, G., Hunt, S.P., Richter-Levin, G.,  
 Mallet, J., Laroche, S. and Blais, T.V.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre,  
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 SOURCE  
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 O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V., De  
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 Laroche S., Bliss T.V.P. and French P.U. Differential Amplification of Intron-containing Transcripts Reveals  
 Long Term Potentiation-associated Up-regulation of Specific Pde10A  
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 J. Biol. Chem. 279 (16), 15841-15849 (2004)  
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## ORIGIN

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 REFERENCE 1 (bases 1 to 3353)  
 O'Connor, V., Genin, A., Davis, S., Karishma, K.K., Doyere, V., De  
 Zeeuw, C.I., Sanger, G., Hunt, S.P., Richter-Levin, G., Maillet, J.,  
 Laroche, S., Bliss, T.V.P. and French, P.J. Differential Amplification of Intron-containing Transcripts Reveals  
 Long Term Potentiation-associated Up-regulation of Specific Pde10A  
 Phosphodiesterase Splice Variants  
 J. Biol. Chem. 279 (16), 15841-15849 (2004)  
 1475215  
 JOURNAL PUBLISHED 2 (bases 1 to 3353)  
 REFERENCES French, P.J., O'Connor, V., Genin, A., Davis, S., Karishma, K.K.,  
 Doyere, V., de Zeeuw, C., Sanger, G., Hunt, S.P., Richter-Levin, G.,  
 Maillet, J., Laroche, S. and Bliss, T.V.P.  
 AUTHORS Direct Submission  
 TITLE Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre,  
 JOURNAL

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 VERSION AF127480.1 GI:4894716  
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 Louhney,K., Snyder,P.B., Uher,L., Roseman,G.J., Ferguson,K. and  
 Florio,V.A.  
 Isolation and characterization of PDE10A, a novel human 3',  
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 Gene 234 (1), 109-117 (1999)  
 JOURNAL  
 PUBMED 2 (bases 1 to 4401)  
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 Louhney,K., Snyder,P.B., Uher,L., Roseman,G.J., Ferguson,K. and  
 Florio,V.A.  
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 QY 2742 GGAAGAGTAAATTCGCGGGGAGAGACAGCAATGTGATTTCAAGGCCAGGCCCGGCGC 2801  
 DB 2341 GGAAGAGTAAATTCGAGGGGAGAGACTGCACCTGGAATTTCAATCCCAATCCGCGGCTC 2400

Search completed: January 12, 2006, 08:50:41  
 Job time : 17779 secs



XX Claim 4; Page 68-70; 158bp; English.

CC The present sequence encodes a murine phosphodiesterase enzyme,  
CC designated PDE11. PDE11 sequences from human and rat are also disclosed.  
CC PDE11 is found in the striatum and corpus cavernosum. PDE11 is believed  
CC to catalyze the conversion of cGMP to GMP. As cGMP is the messenger in  
CC the male erectile process, inhibiting the activity of PDE11 is likely to  
CC increase the concentration of cGMP and so enhance the male erectile  
CC process. The PDE11 enzymes are used in assays for identifying agents  
CC which can affect PDE11 activity or expression. They are also used to  
CC screen for agents useful in the treatment of sexual dysfunction. The  
CC identified agent can be used in a pharmaceutical compositions to treat a  
CC disease or condition associated with PDE11. A PDE11 gene or expression  
CC product can be used to prepare a medicament for the treatment or  
CC modulation of disturbances associated with a PDE11 imbalance. The gene or  
CC expression product can also be used to screen for modulators of PDE11  
CC activity or expression

XX Sequence 3606 BP; 861 A; 1013 C; 962 G; 770 T; 0 U; 0 Other;

Query Match 100.0%; Score 3606; DB 3; Length 3606;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCGCTCCGCTCTCATCTGCTCTTCCACCTCCCGCGCGCTCTCCGAGAAAGGAGGCGC 60  
DB 1 AGCGCTCCGCTCTCATCTGCTCTTCCACCTCCCGCGCGCTCTCCGAGAAAGGAGGCGC 60  
QY 61 AGCGCGCGCTGAGAGAGAGAGAGAGCGCGCGCGCGATGCTGCGCGCGCGCGAGAG 120  
DB 61 AGCGCGCGCTGAGAGAGAGAGAGAGCGCGCGCGCGCGATGCTGCGCGCGCGCGAGAG 120  
QY 121 AGGACAAAGAGAGAGCTCCCTTGAAGCTCCCGCGAGAGTCAACCGAGAGAGCGGTGG 180  
DB 121 AGGACAAAGAGAGAGCTCCCTTGAAGCTCCCGCGAGAGTCAACCGAGAGAGCGGTGG 180  
QY 121 AGGACAAAGAGAGAGCTCCCTTGAAGCTCCCGCGAGAGTCAACCGAGAGAGCGGTGG 180  
DB 121 AGGACAAAGAGAGAGCTCCCTTGAAGCTCCCGCGAGAGTCAACCGAGAGAGCGGTGG 180  
QY 181 CAGAGCGGTGGCAACGCGCGCGCGCGCGCTCTCTCTGCGCTGCGCATTCAAAGGCTT 240  
DB 181 CAGAGCGGTGGCAACGCGCGCGCGCGCGCTCTCTCTGCGCTGCGCATTCAAAGGCTT 240  
QY 181 CAGAGCGGTGGCAACGCGCGCGCGCGCGCTCTCTCTGCGCTGCGCATTCAAAGGCTT 240  
DB 181 CAGAGCGGTGGCAACGCGCGCGCGCGCGCTCTCTCTGCGCTGCGCATTCAAAGGCTT 240  
QY 241 GCTGCTCTCTGCGCGCGCGCGCGCGCGCATCTCCGCGCGCGCTTCCCTTACACC 300  
DB 241 GCTGCTCTCTGCGCGCGCGCGCGCGCGCATCTCCGCGCGCGCTTCCCTTACACC 300  
QY 301 GGGTGCACGCGCGCGGACTCTCGGAATTTTCGGGCGCGCGGCGGCTGCGCT 360  
DB 301 GGGTGCACGCGCGCGGACTCTCGGAATTTTCGGGCGCGCGGCGGCTGCGCT 360  
QY 361 CGGCGCGCGCTCTGCGCGCGCGCGCGCATCTTTGGCGCGCGCGCGCGCTTCCC 420  
DB 361 CGGCGCGCGCTCTGCGCGCGCGCGCGCATCTTTGGCGCGCGCGCGCGCTTCCC 420  
QY 421 CTTTGCACCGGTTTGGCGCGCTCCCTTGGGCTCGGACATGAGAAAGTGAACCTTTACAA 480  
DB 421 CTTTGCACCGGTTTGGCGCGCTCCCTTGGGCTCGGACATGAGAAAGTGAACCTTTACAA 480  
QY 481 TCGGAGTTGCTTCCGAAAGCTGACCGAGTGTTCCTCAGCGCGCGCGAGTTGAACGATGAAA 540  
DB 481 TCGGAGTTGCTTCCGAAAGCTGACCGAGTGTTCCTCAGCGCGCGCGAGTTGAACGATGAAA 540  
QY 541 GGTGAAGGCTATCTTTCTCTCCATCCCGAGGTATTAAGTAATTTGTTTTCGAAAGGT 600  
DB 541 GGTGAAGGCTATCTTTCTCTCCATCCCGAGGTATTAAGTAATTTGTTTTCGAAAGGT 600  
QY 601 TAGTGCAGAGACTGTGAGAAAGTGGCTGAAGAGAAACCAACAAAGCAAGATGAAC 660  
DB 601 TAGTGCAGAGACTGTGAGAAAGTGGCTGAAGAGAAACCAACAAAGCAAGATGAAC 660  
QY 661 ATCTCCCAAGAGAGTCAAGAGGTACAGAGTACGAAATGCAAGAGAGTGTGTACAGCT 720  
DB 661 ATCTCCCAAGAGAGTCAAGAGGTACAGAGTACGAAATGCAAGAGAGTGTGTACAGCT 720

QY 721 GAACAGCTTACATAGAGAGCGGCTTGACACGCGCGGAGCAACACACTGCTCTCTATGA 780  
DB 721 GAACAGCTTACATAGAGAGCGGCTTGACACGCGCGGAGCAACACACTGCTCTCTATGA 780  
QY 781 GCTCAGAGCATCATCAGAGATAGCCCAAAAGCGAGATTTGCACTGTACTTCTTGG 840  
DB 781 GCTCAGAGCATCATCAGAGATAGCCCAAAAGCGAGATTTGCACTGTACTTCTTGG 840  
QY 841 AGAGTGCATTAATAGCTGTGTGTGTATACACCCCGGATGAAAGAGCCCAACCCCG 900  
DB 841 AGAGTGCATTAATAGCTGTGTGTGTATACACCCCGGATGAAAGAGCCCAACCCCG 900  
QY 901 GCTCATCCCTGAGAGGCGCATCACCCAGAGTACACATCTCTGCTCTAGTGGCCAAATC 960  
DB 901 GCTCATCCCTGAGAGGCGCATCACCCAGAGTACACATCTCTGCTCTAGTGGCCAAATC 960  
QY 961 TAGGAAAGCGTTGTTGTAAGAGATATCCTTGGGAGTAGGCGATTTCTCGAGTACTGG 1020  
DB 961 TAGGAAAGCGTTGTTGTAAGAGATATCCTTGGGAGTAGGCGATTTCTCGAGTACTGG 1020  
QY 1021 CCTGGAATCAGAAACCGGCATCCAGTCTGTCTTGTGCTTGGCCATGTGCACTTGG 1080  
DB 1021 CCTGGAATCAGAAACCGGCATCCAGTCTGTCTTGTGCTTGGCCATGTGCACTTGG 1080  
QY 1081 AGACTTGAATTGCAATCCTTGAACGTATACAGGCACTGGGAGCAAGAGGCTTCTGCTCAG 1140  
DB 1081 AGACTTGAATTGCAATCCTTGAACGTATACAGGCACTGGGAGCAAGAGGCTTCTGCTCAG 1140  
QY 1141 CCATCAGAGAGTTGCAACAGCAATCTTGTGGGCTTCCGTAGCAATACACAGGTGCA 1200  
DB 1141 CCATCAGAGAGTTGCAACAGCAATCTTGTGGGCTTCCGTAGCAATACACAGGTGCA 1200  
QY 1201 GGTGTGTAGAGTCTCCGCAACAGACCGAACTGAATGACTTCTTCTGACGATACAA 1260  
DB 1201 GGTGTGTAGAGTCTCCGCAACAGACCGAACTGAATGACTTCTTCTGACGATACAA 1260  
QY 1261 GACATCTTGTATATACATAGTTGCGATAGACTCTCTTCTTGAACATCATGATATATGC 1320  
DB 1261 GACATCTTGTATATACATAGTTGCGATAGACTCTCTTCTTGAACATCATGATATATGC 1320  
QY 1321 AAAAAATCTAGTGAACGCGGACGCGTGGCGCTCTTCCAGGTGACCAACAGAA 1380  
DB 1321 AAAAAATCTAGTGAACGCGGACGCGTGGCGCTCTTCCAGGTGACCAACAGAA 1380  
QY 1381 GCTGTATCTCGACCTGTTTGAATTTGGGAGAGAGAGAGGAGGCCATCTTCAAGAA 1440  
DB 1381 GCTGTATCTCGACCTGTTTGAATTTGGGAGAGAGAGAGGAGGCCATCTTCAAGAA 1440  
QY 1441 GACCAAGAGATCAGATTTTCCATTGAGAAAGGAGTTGCTGCTCAAGTGGCAAGAACAG 1500  
DB 1441 GACCAAGAGATCAGATTTTCCATTGAGAAAGGAGTTGCTGCTCAAGTGGCAAGAACAG 1500  
QY 1501 CGAAGTCTTGAACATTCGCCGATGCTACGCGAACCTCGCTTTAACAGAGAGTGAACCT 1560  
DB 1501 CGAAGTCTTGAACATTCGCCGATGCTACGCGAACCTCGCTTTAACAGAGAGTGAACCT 1560  
QY 1561 GTACACAGGCTTACACACAGAGAAACATTTCTGTATGCGCCATAGTGAAGCCAGGAGGT 1620  
DB 1561 GTACACAGGCTTACACACAGAGAAACATTTCTGTATGCGCCATAGTGAAGCCAGGAGGT 1620  
QY 1621 GATTGGCGGTGTGAGATGTGAAACAAGATGAGGAGTGAAGGCTTCTCAGAGACAGACA 1680  
DB 1621 GATTGGCGGTGTGAGATGTGAAACAAGATGAGGAGTGAAGGCTTCTCAGAGACAGACA 1680  
QY 1681 GAACAACCTTCAAGATGTTTGTCTTCTTGGCACTGGCTTGGCACTGTGTCAACATGTA 1740  
DB 1681 GAACAACCTTCAAGATGTTTGTCTTCTTGGCACTGGCTTGGCACTGTGTCAACATGTA 1740  
QY 1741 CCAAGAGATCCGCACTCAAGATGATATCAAGGTTTACATGAGAGAACTTTCTTACCA 1800  
DB 1741 CCAAGAGATCCGCACTCAAGATGATATCAAGGTTTACATGAGAGAACTTTCTTACCA 1800  
QY 1801 CAGATCTGACCTCCGAGAGAGTGGCAAGGCTCATAGGCTTCAACCTACAGACGCGAT 1860



Dbb	1801	CAGCATCTGCACTCCGAGAGTGGCAAGGCGCTCATGCGCTTCAACTCAGCAGCAT	1860
Oy	1861	CTGCCGGGACATCGAGCTATTCACATTGACATATGGTCCCTTCGAGAACATGTGCGCTGG	1920
Dbb	1861	CTGCGGGGACATCGAGCTATTCACATTGACATATGGTCCCTTCGAGAACATGTGCGCTGG	1920
Oy	1921	GATCTTTGTCTACATGATCATCTGGTCTGTGGGACATCTGTCTTTGAACTTGAATAAT	1980
Dbb	1921	GATCTTTGTCTACATGATCATCTGGTCTGTGGGACATCTGTCTTTGAACTTGAATAAT	1980
Oy	1981	GGGCGGTTTTATCATGTCGTGTGAAGAAGACATATCGCGGGGTTCTTTACCACAACTGGAA	2040
Dbb	1981	GGGCGGTTTTATCATGTCGTGTGAAGAAGACATATCGCGGGGTTCTTTACCACAACTGGAA	2040
Oy	2041	GCATGAGCTACCGGTGGCACATCGATGTATGTGCATATCTTCAAAACAAATGGCGCTTT	2100
Dbb	2041	GCATGAGCTACCGGTGGCACATCGATGTATGTGCATATCTTCAAAACAAATGGCGCTTT	2100
Oy	2101	CACAGACCTCGAGCGGAAGGCGCTGTATATGCGTGTCTGTGCAATGACTGGACACAG	2160
Dbb	2101	CACAGACCTCGAGCGGAAGGCGCTGTATATGCGTGTCTGTGCAATGACTGGACACAG	2160
Oy	2161	GGGCTTCAGTACAGCTACCTGAGAAAGTTGCACACCCCTGGCGGCGGTGATCTCAC	2220
Dbb	2161	GGGCTTCAGTACAGCTACCTGAGAAAGTTGCACACCCCTGGCGGCGGTGATCTCAC	2220
Oy	2221	CTGCACATGAGACAAACACACTTCTCCGAGCGGTGCATCTTCACGCTGAGAGGGCA	2280
Dbb	2221	CTGCACATGAGACAAACACACTTCTCCGAGCGGTGCATCTTCACGCTGAGAGGGCA	2280
Oy	2281	CAATATCTTCTCCAGCCCTGAGCTTCAGAGATACAGCAGGTGCTGGAGATCATCGCAA	2340
Dbb	2281	CAATATCTTCTCCAGCCCTGAGCTTCAGAGATACAGCAGGTGCTGGAGATCATCGCAA	2340
Oy	2341	AGCCATCATGCGCACCGGACCTTGGCGCTTATCTTTGGGAAACAGGAAGAGTTGAGAGAT	2400
Dbb	2341	AGCCATCATGCGCACCGGACCTTGGCGCTTATCTTTGGGAAACAGGAAGAGTTGAGAGAT	2400
Oy	2401	GTACACAGACAGGGTGGCTGAACCTCCACAACAGATCCCATCGAGACCGGTCAATCGGCTT	2460
Dbb	2401	GTACACAGACAGGGTGGCTGAACCTCCACAACAGATCCCATCGAGACCGGTCAATCGGCTT	2460
Oy	2461	GATGATGACTGCTGTGATCTTTGCTGTGACCAAACTATGGCAGATTAACAATTTGAC	2520
Dbb	2461	GATGATGACTGCTGTGATCTTTGCTGTGACCAAACTATGGCAGATTAACAATTTGAC	2520
Oy	2521	AGCGATGATATATATGCAGAAATCTGGGGCTGAGGGGTGATGAGATGAAGAAGCTGGGCAT	2580
Dbb	2521	AGCGATGATATATATGCAGAAATCTGGGGCTGAGGGGTGATGAGATGAAGAAGCTGGGCAT	2580
Oy	2581	ACAGCCCAATTCCTATGATNGGACAGAGACAAGCGAGATGAAGTCCCTCAAGGGGACGCTCGG	2640
Dbb	2581	ACAGCCCAATTCCTATGATNGGACAGAGACAAGCGAGATGAAGTCCCTCAAGGGGACGCTCGG	2640
Oy	2641	ATTCTTCAATGCTGTGACCAATTCGCTCTATACCACTTGAACGAGATCTCTCCACCCAC	2700
Dbb	2641	ATTCTTCAATGCTGTGACCAATTCGCTCTATACCACTTGAACGAGATCTCTCCACCCAC	2700
Oy	2701	AGAGCCTCTGCTGAAGGCTGACAGGATTAACCTCAATCAGTGGGAGGAAGTAAATTCGCGG	2760
Dbb	2701	AGAGCCTCTGCTGAAGGCTGACAGGATTAACCTCAATCAGTGGGAGGAAGTAAATTCGCGG	2760
Oy	2761	GGAAGAGACAGCAATGTGCAATTTCAAGGCCACAGGCCCGGCTGAGCAAGACACACCTGA	2820
Dbb	2761	GGAAGAGACAGCAATGTGCAATTTCAAGGCCACAGGCCCGGCTGAGCAAGACACACCTGA	2820
Oy	2821	GAACTGTAACGTGAAGTGTGAAGACTGATCTCTGAAGTGAACGTCCTGATGTCTGGCCACGA	2880
Dbb	2821	GAACTGTAACGTGAAGTGTGAAGACTGATCTCTGAAGTGAACGTCCTGATGTCTGGCCACGA	2880
Oy	2881	ACCGACTCAACCTGCTTGTGACTTGGTCTTTTGTTCGAAGGGTGAAAACCCCTT	2940
Dbb	2881	ACCGACTCAACCTGCTTGTGACTTGGTCTTTTGTTCGAAGGGTGAAAACCCCTT	2940

Db	2881	ACGCACTCAACCTGCTTCTGTGACTTGCTCTTTTGTTTTCAAGGGGTGAAAAACCCCT	2944
Qy	2941	GTGAGAAAGTACCGTGCATATTCATGTGAAGCAGACGACTCCCTGTTGCCCAAC	3000
Db	2941	GTGAGAAAGTACCGTGCATATTCATGTGAAGCAGACGACTCCCTGTTGCCCAAC	3000
Qy	3001	CTGGAACAGTGAACAAACCCAGGCTGCGGTTCAGACGTGGGCTACTCCGTGGCTCA	3060
Db	3001	CTGGAACAGTGAACAAACCCAGGCTGCGGTTCAGACGTGGGCTACTCCGTGGCTCA	3060
Qy	3061	CTGACCTCCGAATGCTATTGCTGCCAGGCACTGCACTGTGAGGGGGCAGAG	3120
Db	3061	CTGACCTCCGAATGCTATTGCTGCCAGGCACTGCACTGTGAGGGGGCAGAG	3120
Qy	3121	ACCAAGAGAGGTTCTTTCCTGCTGATCTCTCCATGAGGGTGTGGCCAGTCCCTGGTTCT	3180
Db	3121	ACCAAGAGAGGTTCTTTCCTGCTGATCTCTCCATGAGGGTGTGGCCAGTCCCTGGTTCT	3180
Qy	3181	GTGCGATGCTGCTGCTTGTGGGCACTGGTTAGGAATGGGCAACAGGCCCTTGTGTGA	3240
Db	3181	GTGCGAAGCTGCTGCTTGTGGGCACTGGTTAGGAATGGGCAACAGGCCCTTGTGTGA	3240
Qy	3241	GTTTACATGTGACCTTCTTAAGGTTAACTGAGTTGTGGCTGGGACACATGTATGAA	3300
Db	3241	GTTTACATGTGACCTTCTTAAGGTTAACTGAGTTGTGGCTGGGACACATGTATGAA	3300
Qy	3301	GGTCACAGTCCACAGGTGACAGAGAAATCCAACTGTATTATCAAGTGCACTACAGTA	3360
Db	3301	GGTCACAGTCCACAGGTGACAGAGAAATCCAACTGTATTATCAAGTGCACTACAGTA	3360
Qy	3361	TGCTCTTTCAAGTCTATCTGCGGGGCACTAGGTGAGTGTGCTCCACTGAGAGAACATA	3420
Db	3361	TGCTCTTTCAAGTCTATCTGCGGGGCACTAGGTGAGTGTGCTCCACTGAGAGAACATA	3420
Qy	3421	CCTTCGCCCTCATCCAGGGGACACAGGGTACATCCAGGCACTCGGGAACTGAAGCTTC	3480
Db	3421	CCTTCGCCCTCATCCAGGGGACACAGGGTACATCCAGGCACTCGGGAACTGAAGCTTC	3480
Qy	3481	ACTTCAAACCATGTCAAAAGATTAAAAACCTCCCTCCCTCACTGTAGCCTTGGCA	3540
Db	3481	ACTTCAAACCATGTCAAAAGATTAAAAACCTCCCTCCCTCACTGTAGCCTTGGCA	3540
Qy	3541	ACTGCGCCATCCCTTTATACAAAGAAATTAAGTAAAGGATATTAATTTAAAAAAA	3600
Db	3541	ACTGCGCCATCCCTTTATACAAAGAAATTAAGTAAAGGATATTAATTTAAAAAAA	3600
Qy	3601	AAAAAA 3606	
Db	3601	AAAAAA 3606	
RESULT 2			
AAFB5097			
ID	AAFB5097	standard; cDNA; 7618 BP.	
AC	AAFB5097;		
XX			
XX			
DT	09-JUL-2001	(first entry)	
XX			
DE	Nucleotide sequence of murine PDB10A gene cDNA clone.		
XX			
KW	PDB10A gene; striatum; CAG repeat disorder; Huntington's disease;		
KW	Schizophrenia; Alzheimer's disease; Parkinson's disease; stroke; trauma;		
KW	de.		
OS	Mus sp.		
XX			
PN	WO200124781-A2.		
XX			
PD	12-APR-2001.		
PF	06-OCT-2000; 2000WO-CA001188.		
XX			

PR 07-OCT-1999; 99CA-02285690.  
PR 07-OCT-1999; 99US-0158043P.  
PR 12-JUL-2000; 2000US-0217765P.  
XX  
XX  
PA (NOVA-) NOVANEURON INC.  
PI Robertson HA, Denovan-Wright EM;  
XX  
XX WPI: 2001-308190/32.  
DR  
PT Novel composition for treating CAG repeat disorder such as Huntington's  
XX disease, comprises a compound which modulates PDE10A expression.  
XX  
XX Example 5; Fig 19; 143pp; English.  
CC The present sequence represents a cloned PDE10A polynucleotide. PDE10A is  
CC a gene that is normally highly expressed in mammalian striatum.  
CC Expression of this gene decreases during development of CAG repeat  
CC disorders. Quantification of expression of the PDE10A gene is useful for  
CC detecting the presence of or predisposition for a CAG repeat disorder.  
CC Compounds which modulate PDE10A expression are used for treating a CAG  
CC repeat disorder, e.g. Huntington's disease, schizophrenia, Alzheimer's  
CC disease, Parkinson's disease, stroke and trauma  
XX  
XX Sequence 7618 BP; 2062 A; 1802 C; 1764 G; 1986 T; 0 U; 4 Other;  
SQ  
Query Match 85.0%; Score 3064; DB 4; Length 7618;  
Beet Local Similarity 99.6%; Pred. No. 0;  
Matches 3070; Conservative 1; Mismatches 11; Indels 0; Gaps 0;  
QY 525 GTTTAGCGATGAAAAGTGAAGGCTATCTTCTCTCCATCCCGAGTATTAGAT 584  
DB 273 GTTTACCGATGAAAAGTGAAGGCTATCTTCTCTCCATCCCGAGTATTAGAT 332  
QY 585 TTGTTTCTGAAAGTGTAGTGAAGACTGTGTGAAAAGTGGCTGAAGAGAAAACCA 644  
DB 333 TTGTTTCTGAAAGTGTAGTGAAGACTGTGTGAAAAGTGGCTGAAGAGAAAACCA 392  
QY 645 AAGCAAAAGATGAACATCTCCCAAGGAAGTGAAGCAAGTACAGATTAAGATAGCAG 704  
DB 393 AAGCAAAAGATGAACATCTCCCAAGGAAGTGAAGCAAGTACAGATTAAGATAGCAG 452  
QY 705 GAGTGTGACAGGTGAACAGCTACATAGACAGCGCTGGAACAAGCGGGGACAACC 764  
DB 453 GAGTGTGACAGGTGAACAGCTACATAGACAGCGCTGGAACAAGCGGGGACAACC 512  
QY 765 ACTGTCTCTATAGACTCAGACAGATCATAGATAGCCCAAAAAGCCGAGATTGG 824  
DB 513 ACTGTCTCTATAGACTCAGACAGATCATAGATAGCCCAAAAAGCCGAGATTGG 572  
QY 825 CACTGTACTCTCTGGAAGTGAAGTAATAGCTGTGTGTTCATACACCGGGATGA 884  
DB 573 CACTGTACTCTCTGGAAGTGAAGTAATAGCTGTGTGTTCATACACCGGGATGA 632  
QY 885 AGGAAGCCCAACCCCGCTCATCTGCAAGGCCCATCAACGAGGTACCAACATCTCTG 944  
DB 633 AGGAAGCCCAACCCCGCTCATCTGCAAGGCCCATCAACGAGGTACCAACATCTCTG 692  
QY 945 CCTACGTGCGCAAGTCTAGAGAGAGCGTTGTGTAGAGATATCTTGGGAGTAGCCAT 1004  
DB 693 CCTACGTGCGCAAGTCTAGAGAGAGCGTTGTGTAGAGATATCTTGGGAGTAGCCAT 752  
QY 1005 TTCTCTGAGATCTAGGCTTGAATAGAAACCCGATCCAGTCTTCTTGGCTGGCCA 1064  
DB 753 TTCTCTGAGATCTAGGCTTGAATAGAAACCCGATCCAGTCTTCTTGGCTGGCCA 812  
QY 1065 TTGTCACTGCACTTGAAGCTTGAATGAGCATCTTGAACGTACAGGCACTGGGCAAG 1124  
DB 813 TTGTCACTGCACTTGAAGCTTGAATGAGCATCTTGAACGTACAGGCACTGGGCAAG 872  
QY 1125 AGGCTTCTGCTCAGCATCAGAGGTTGCAACAGCCCATCTTGGGCTTCGGTAG 1184  
DB 873 AGGCTTCTGCTCAGCATCAGAGGTTGCAACAGCCCATCTTGGGCTTCGGTAG 932

QY 1185 CAATACACAGGTGAGGTGTGTAGAGGTCTGCGCAACAGACCGAATGATGACTTCC 1244  
DB 933 CAATACACAGGTGAGGTGTGTAGAGGTCTGCGCAACAGACCGAATGATGACTTCC 992  
QY 1245 TACTGACGTATCAAGACATCTTTGATTAACATATGTTCCATAGACTCTTACTTGAAC 1304  
DB 993 TACTGACGTATCAAGACATCTTTGATTAACATATGTTCCATAGACTCTTACTTGAAC 1052  
QY 1305 ACATCATATATATGCAAAAAATCTAGTAACCGCGACCGCGCTCTTCCAGTGG 1364  
DB 1053 ACATCATATATATGCAAAAAATCTAGTAACCGCGACCGCGCTCTTCCAGTGG 1112  
QY 1365 ACCACAAGAACAGAGGCTGTACTGAGACTGTGTAATTTGATTTGGGAGAGAGAGGGA 1424  
DB 1113 ACCACAAGAACAGAGGCTGTACTGAGACTGTGTAATTTGATTTGGGAGAGAGAGGGA 1172  
QY 1425 AGCCATCTTCAAGAAACCAAGAGATCAATTTCCATTGAGAAAGGATTTGCTGTC 1484  
DB 1173 AGCCATCTTCAAGAAACCAAGAGATCAATTTCCATTGAGAAAGGATTTGCTGTC 1232  
QY 1485 AAGTGCAGAAACAGGCGAAGTCTTGAACTTTCCGATGCTACGCGGACCTGCTTTA 1544  
DB 1233 AAGTGCAGAAACAGGCGAAGTCTTGAACTTTCCGATGCTACGCGGACCTGCTTTA 1292  
QY 1545 ACAGGAGGTGAGCTGTACACAGGCTACACACAGAGAACTTCTGTATGCCCATAG 1604  
DB 1293 ACAGGAGGTGAGCTGTACACAGGCTACACACAGAGAACTTCTGTATGCCCATAG 1352  
QY 1605 TGAGCGGAGGACGCTGATTTGGCGTGTGTGAGATGTGAACAAGATCAGCGGTAGCGCT 1664  
DB 1353 TGAGCGGAGGACGCTGATTTGGCGTGTGTGAGATGTGAACAAGATCAGCGGTAGCGCT 1412  
QY 1665 TCTCCAAACAGACGAGAACTTCAAGATTTTCTGTCTTCTGCGCACTGGCTTGC 1724  
DB 1413 TCTCCAAACAGACGAGAACTTCAAGATTTTCTGTCTTCTGCGCACTGGCTTGC 1472  
QY 1725 ACTGTCTAACTGATACACAGATCCGCACTCAGATGATCTACAGGGTTACATGG 1784  
DB 1473 ACTGTCTAACTGATACACAGATCCGCACTCAGATGATCTACAGGGTTACATGG 1532  
QY 1785 AGAAGCTTCTTACACAGATCTGACCTGACCTGAGAGTGCAGAGCTCATGCGCTTCA 1844  
DB 1533 AGAAGCTTCTTACACAGATCTGACCTGACCTGAGAGTGCAGAGCTCATGCGCTTCA 1592  
QY 1845 ACTTACAGACAGATCTGCGCGGACATCGAGCTATTCCAATTGACATTTGCTCTTGC 1904  
DB 1593 ACTTACAGACAGATCTGCGCGGACATCGAGCTATTCCAATTGACATTTGCTCTTGC 1652  
QY 1905 AGAATGATGGCTGGGATCTTGTCTTACATGATCCATCGGCTTGGGACATCTGTT 1964  
DB 1653 AGAATGATGGCTGGGATCTTGTCTTACATGATCCATCGGCTTGGGACATCTGTT 1712  
QY 1965 TTGAATCTGAAAAATTTGCGCGTTTATCATGTCTGTGAAGAAACTATCGCGGTTTC 2024  
DB 1713 TTGAATCTGAAAAATTTGCGCGTTTATCATGTCTGTGAAGAAACTATCGCGGTTTC 1772  
QY 2025 CTTACCAAACTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2084  
DB 1773 CTTACCAAACTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1832  
QY 2085 ACAACATGAGCTCTTACAGACCTGAGCGCAAAAGGCTCTTATTTGCGTGTGCTGCC 2144  
DB 1833 ACAACATGAGCTCTTACAGACCTGAGCGCAAAAGGCTCTTATTTGCGTGTGCTGCC 1892  
QY 2145 ATGACCTTGACACAGGGGCTTCACTAAGCTACCTGAGAGTTGACACACCCCTGCG 2204  
DB 1893 ATGACCTTGACACAGGGGCTTCACTAAGCTACCTGAGAGTTGACACACCCCTGCG 1952  
QY 2205 CGGCGCTTACTTCACTTCCACATGAGCAACACATTTCTCCAGACGCTGTCATCC 2264  
DB 1953 CGGCGCTTACTTCACTTCCACATGAGCAACACATTTCTCCAGACGCTGTCATCC 2012



QY 2265 TTCACTGGAGGGGCAATATCTTCTCACTCTGAGCTCCAGCGAGTACAGCAGGTCC 2324  
DB 2013 TTCACTGGAGGGGCAATATCTTCTCACTCTGAGCTCCAGCGAGTACAGCAGGTCC 2072  
QY 2335 TGGAGATCATCCGCAAGGCAATATGCGCACTGCACTCCGCTCTTATCTTTGGGAAACAGA 2384  
DB 2073 TGGAGATCATCCGCAAGGCAATATGCGCACTGCACTCCGCTCTTATCTTTGGGAAACAGA 2132  
QY 2385 AGCAGTTGGAGGAGATGTACAGAGCAGGCTGCTGAACTCTCAACAACAGTCCATCGAG 2444  
DB 2133 AGCAGTTGGAGGAGATGTACAGAGCAGGCTGCTGAACTCTCTCAACAACAGTCCATCGAG 2192  
QY 2445 ACCGCTCATCCGCTTATGATGATGATGCTGCTGATCTTTTCTGTGACCAATCTATGCGC 2504  
DB 2193 ACCGCTCATCCGCTTATGATGATGATGCTGCTGATCTTTTCTGTGACCAATCTATGCGC 2252  
QY 2505 CAGTTACAAAATTTGACAGGGAATGATATATATCCAAATTTCTGGGGGTGAGGGGATGAGA 2564  
DB 2253 CAGTTACAAAATTTGACAGGGAATGATATATATCCAAATTTCTGGGGGTGAGGGGATGAGA 2312  
QY 2565 TGAAGAAAGTGGGATACAGCCCAATCTATGATGAGCAGAGACAAGAGAGATGAAGTCC 2624  
DB 2313 TGAAGAAAGTGGGATACAGCCCAATCTATGATGAGCAGAGACAAGAGAGATGAAGTCC 2372  
QY 2625 CTCAAGGGGAGCTCGGATTTCTCAATGCTGTGCGCAATCCCTGCTATACCACTTGAACGC 2684  
DB 2373 CTCAAGGGGAGCTCGGATTTCTCAATGCTGTGCGCAATCCCTGCTATACCACTTGAACGC 2432  
QY 2685 AGATCTCTCCCAACCAAGAGCTCTGTGAAAGGCTGCAAGGGATTAACCTCAACACTGGGG 2744  
DB 2433 AGATCTCTCCCAACCAAGAGCTCTGTGAAAGGCTGCAAGGGATTAACCTCAACACTGGGG 2492  
QY 2745 AGAAGGTAATTTGCGGGGGAAGAGACAGCAATGTGATTTGAGGCCAGGCCCGCGCCCTTA 2804  
DB 2493 AGAAGGTAATTTGCGGGGGAAGAGACAGCAATGTGATTTGAGGCCAGGCCCGCGCCCTTA 2552  
QY 2805 GCAAGAGCACACCTGAGAAAGCTGAACGTGAAGGTTGAAAGCTGATCTGAACTGAGCTCC 2864  
DB 2553 GCAAGAGCACACCTGAGAAAGCTGAACGTGAAGGTTGAAAGCTGATCTGAACTGAGCTCC 2612  
QY 2865 TGATGTCTGCGCCAGCAACCGATCTCAACTCTCTGTGACTTGGTCTTTTGTCTTTCGA 2924  
DB 2613 TGATGTCTGCGCCAGCAACCGATCTCAACTCTCTGTGACTTGGTCTTTTGTCTTTCGA 2672  
QY 2925 GGGGTGAACCCCTGTCAGAAAGTACCGTGCATATCCATGTGAAGCAGACGACTCCC 2984  
DB 2673 GGGGTGAACCCCTGTCAGAAAGTACCGTGCATATCCATGTGAAGCAGACGACTCCC 2732  
QY 2985 TGCCTGCGGACACACCTCGGACAGTGAAGCAACCAAGCTCTGCGCTGTTCAAGCTGCG 3044  
DB 2733 TGCCTGCGGACACACCTCGGACAGTGAAGCAACCAAGCTCTGCGCTGTTCAAGCTGCG 2792  
QY 3045 CTACTCGTGGCTTCACCTGACTCTCCGAATGCTATTTGCTCCAGGGCAGACGTCGACTG 3104  
DB 2793 CTACTCGTGGCTTCACCTGACTCTCCGAATGCTATTTGCTCCAGGGCAGACGTCGACTG 2852  
QY 3105 TCTGGAAGGGGCGAGAGCCAGAGAGGTTCTTCCCTGACATCTCCCATGAGGGGTGTGG 3164  
DB 2853 TCTGGAAGGGGCGAGAGCCAGAGAGGTTCTTCCCTGACATCTCCCATGAGGGGTGTGG 2912  
QY 3165 CCAAGTTCCTGAGTCTGTGCAATGCTGTGCTGGTGGTGAATGTTGTTAGAAATGGAACACA 3224  
DB 2913 CCAAGTTCCTGAGTCTGTGCAATGCTGTGCTGGTGGTGAATGTTGTTAGAAATGGAACACA 2972  
QY 3225 CGCCCTGTTGTGAAGTTTACATGTTGACCTTTCTTATAGTTTAACTGAGTTTGGGCTG 3284  
DB 2973 CGCCCTGTTGTGAAGTTTACATGTTGACCTTTCTTATAGTTTAACTGAGTTTGGGCTG 3032  
QY 3285 GGAACATGTATATGAAGTCAAGTCCACAGTGAACAGAAATCCAAACTGTGATTAAC 3344  
DB 3033 GGAACATGTATATGAAGTCAAGTCCACAGTGAACAGAAATCCAAACTGTGATTAAC 3092  
QY 3345 AGGTGCACTAAGGTATGCTCTTTCAGTCTATCTGGGGGCAATAGGTGAGTCTGCTCA 3404

DB 3093 AGGTGCACTAAGGTATGCTCTTTCAGTCTATCTGGGGGCAATAGGTGAGTCTGCTCA 3152  
QY 3405 CTCAAGAGGAAGCATATCTTGCCTCTATTCAGGGGACACAGGGTACATCCACGAGCATCG 3464  
DB 3153 CTCAAGAGGAAGCATATCTTGCCTCTATTCAGGGGACACAGGGTACATCCACGAGCATCG 3212  
QY 3465 GGGAACTGAAGTCTCATCTTGAACCATGTCAAAAGATTAAACACCTCCCTCCCTC 3524  
DB 3213 GGGAACTGAAGTCTCATCTTGAACCATGTCAAAAGATTAAACACCTCCCTCCCTC 3272  
QY 3525 ACTGTAGCCTTGGGCACTGCGCCCAATCCCTTATACAAAGAAAATAAAGTAAAGCATTA 3584  
DB 3273 ACTGTAGCCTTGGGCACTGCGCCCAATCCCTTATACAAAGAAAATATAGTAAAGCATTA 3332  
QY 3585 TAAATTTAAAAA 3606  
DB 3333 TAAATTTCTCCAGCAAGCAAA 3354

RESULT 3  
ID AAF85096  
AAF85096 standard; cDNA; 7581 BP.  
AC AAF85096;  
XX  
DT 09-JUL-2001 (first entry)  
XX  
DB Nucleotide sequence of murine PDE10A gene cDNA clone cpDE10A.  
XX  
KM PDE10A gene; striatum; CAG repeat disorder; Huntington's disease;  
KM Schizophrenia; Alzheimer's disease; Parkinson's disease; stroke; trauma;  
XX ds.  
OS Mus sp.  
XX  
PN MO200124781-A2.  
XX  
PD 12-APR-2001.  
XX  
PF 06-OCT-2000; 2000MO-CA001188.  
XX  
PR 07-OCT-1999; 99CA-02285690.  
PR 07-OCT-1999; 99US-0158043P.  
PR 12-JUL-2000; 2000US-0217765P.  
XX  
PA (NOVA-) NOVANEURON INC.  
XX  
PI Robertson HA, Denovan-Wright EM;  
XX  
DR WPI; 2001-308190/32.  
XX  
PT Novel composition for treating CAG repeat disorder such as Huntington's  
XX disease, comprises a compound which modulates PDE10A expression.  
XX  
PS Example 5; Fig 15; 143bp; English.  
XX  
CC The present sequence represents a cloned PDE10A polynucleotide. PDE10A is  
CC a gene that is normally highly expressed in mammalian striatum.  
CC Expression of this gene decreases during development of CAG repeat  
CC disorders. Quantification of expression of the PDE10A gene is useful for  
CC detecting the presence of or predisposition for a CAG repeat disorder.  
CC Compounds which modulate PDE10A expression are used for treating a CAG  
CC repeat disorder, e.g. Huntington's disease, Schizophrenia, Alzheimer's  
CC disease, Parkinson's disease, stroke and trauma  
XX  
SQ Sequence 7581 BP; 2038 A; 1796 C; 1759 G; 1969 T; 0 U; 19 Other;  
XX  
Query Match 84.6%; Score 3050.4; DB 4; Length 7581;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 3068; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
QY 525 GTTTGACGATGAAAAGGCTATCTTCTCTCCATCCCAAGTATTAATGATGAAT 584

Db 273 GTTGAACGATGAAAAGTGAAGGCTATCTTCTCCATCCCGAGTTATAGTAAT 332  
QY 585 TTGTTTCTGAAAAGTGTAGTGCAGAGACTGTGAAAAAGTGGCTGAAGAGAAAAACCAAC 644  
Db 333 TTGTTTCTGAAAAGTGTAGTGCAGAGACTGTGAAAAAGTGGCTGAAGAGAAAAACCAAC 392  
QY 645 AAGCAAAAATGAAACCATCTCCCAAGAAAGTGCAGAGATTACAGGATTAAGAAATATGCAG 704  
Db 393 AAGCAAAAATGAAACCATCTCCCAAGAAAGTGCAGAGATTACAGGATTAAGAAATATGCAG 452  
QY 705 GAGTCGTACAGAGCTGAACAGCTACATAGAGAGCGCTGGAACAGGGCGGGGACAAAC 764  
Db 453 GAGTCGTACAGAGCTGAACAGCTACATAGAGAGCGCTGGAACAGGGCGGGGACAAAC 512  
QY 765 ACCGTCTCTTAATGAGCTCAGAGCATCATCAGATTAAGCACAAAAGCCAGCATTTG 824  
Db 513 ACCGTCTCTTAATGAGCTCAGAGCATCATCAGATTAAGCACAAAAGCCAGCATTTG 572  
QY 825 CACTGACTTCCCTTGAGAGTGCATTAATAGCCTGTGTGTTGTTCAACACCCGGGATGA 884  
Db 573 CACTGACTTCCCTTGAGAGTGCATTAATAGCCTGTGTGTTGTTCAACACCCGGGATGA 632  
QY 885 AAGAAAGCCAAACCCGGCTCATCCCTGCAGGGCCCATCAACGAGGTACACCATCTCTG 944  
Db 633 AAGAAAGCCAAACCCGGCTCATCCCTGCAGGGCCCATCAACGAGGTACACCATCTCTG 692  
QY 945 CCTAGGTGCCAAGTCTAGAGAAAGCTTTGTGTAGAGAAATCTTGGGGATGAGCGAT 1004  
Db 693 CCTAGGTGCCAAGTCTAGAGAAAGCTTTGTGTAGAGAAATCTTGGGGATGAGCGAT 752  
QY 1005 TTCCCTGAGAGTACTGGCTGGAATCAGAAACCGGCATCCAGTCTGTCTTGGCTGGCCA 1064  
Db 753 TTCCCTGAGAGTACTGGCTGGAATCAGAAACCGGCATCCAGTCTGTCTTGGCTGGCCA 812  
QY 1065 TTGTCACTGCAATTGAGAGCTTGAATTGGCATCTTGAACGTGTACAGGCACTGCGGCAAG 1124  
Db 813 TTGTCACTGCAATTGAGAGCTTGAATTGGCATCTTGAACGTGTACAGGCACTGCGGCAAG 872  
QY 1125 AAGCCTTCTGCTCAGCCATCAGAGAGTTGCAACAGCCAACTTGTGGCTTCCGTG 1184  
Db 873 AAGCCTTCTGCTCAGCCATCAGAGAGTTGCAACAGCCAACTTGTGGCTTCCGTG 932  
QY 1185 CAATACACCAAGGTGAGGTGTAGAGGTCTGCGCAACAGACCGAATCGAATGACTTCC 1244  
Db 933 CAATACACCAAGGTGAGGTGTAGAGGTCTGCGCAACAGACCGAATCGAATGACTTCC 992  
QY 1245 TACTGACGTATCAAGAATCACTTTGATTAAGTATGATGCTCTTAATTGAAC 1304  
Db 993 TACTGACGTATCAAGAATCACTTTGATTAAGTATGATGCTCTTAATTGAAC 1052  
QY 1305 ACATCATGATATATGCAAAAAATCTTAGTGAACGCCGACCGCTGCGCTCTTCAAGTGG 1364  
Db 1053 ACATCATGATATATGCAAAAAATCTTAGTGAACGCCGACCGCTGCGCTCTTCAAGTGG 1112  
QY 1365 ACCAAGAAGAAAGAGCTGTACTGGAACCTGTTTGAACATTTGGGAGAGAAAGAGGGGA 1424  
Db 1113 ACCAAGAAGAAAGAGCTGTACTGGAACCTGTTTGAACATTTGGGAGAGAAAGAGGGGA 1172  
QY 1425 AGCCCATCTTCAAGAAGACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTC 1484  
Db 1173 AGCCCATCTTCAAGAAGACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTC 1232  
QY 1485 AAGTGGCAAGAAACAGCGGAAGTCTTGAAACATTCGCCGATGCTCAGCGGACCTCGCTTTA 1544  
Db 1233 AAGTGGCAAGAAACAGCGGAAGTCTTGAAACATTCGCCGATGCTCAGCGGACCTCGCTTTA 1292  
QY 1545 ACAAGGAGGTGACCTGTATCAAGGCTACACAGAGAGAACTTCTGTGTATGCCCATAG 1604  
Db 1293 ACAAGGAGGTGACCTGTATCAAGGCTACACAGAGAGAACTTCTGTGTATGCCCATAG 1352  
QY 1605 TGAGCCGAGGACGCTGATTTGGCTGTGTGCAATGGTGAACAAGATTACGCGGTAGCGCT 1664

Db 1353 TGAGCCGAGGACGCTGATTTGGCTGTGTGACAGATGTGAACAAGATCAGCGGTAGCGCT 1412  
QY 1665 TTCTCAAGACAGACGAGAACAACTTCAAGATTTTGTCTGTCTTCCGCACTGGCCTTGC 1724  
Db 1413 TTCTCAAGACAGACGAGAACAACTTCAAGATTTTGTCTGTCTTCCGCACTGGCCTTGC 1472  
QY 1725 ACTGTGCTAACATGTATACACAGATCCGCACTCAGAAATGATCTTACAGGGTTACATAG 1784  
Db 1473 ACTGTGCTAACATGTATACACAGATCCGCACTCAGAAATGATCTTACAGGGTTACATAG 1532  
QY 1785 AGAAGCTTTCCTACACAGCATCTGACCTCCGAGAGTGGCAGAGCCTCATGCGCTTCA 1844  
Db 1533 AGAAGCTTTCCTACACAGCATCTGACCTCCGAGAGTGGCAGAGCCTCATGCGCTTCA 1592  
QY 1845 ACCTACAGACGCACTGTGCGGGGACATCGAGCTTATTCACATTTGAACATTTGCTTTCG 1904  
Db 1593 ACCTACAGACGCACTGTGCGGGGACATCGAGCTTATTCACATTTGAACATTTGCTTTCG 1652  
QY 1905 AGAATATGACCTGGATCTTGTCTACATGATCATCGGTCTTGTGGGACATCTGTT 1964  
Db 1653 AGAATATGACCTGGATCTTGTCTACATGATCATCGGTCTTGTGGGACATCTGTT 1712  
QY 1965 TTGAACCTGAAAAATTTGTGCCGTTTATCATGTCTGTGAAGAAATATCGCGGTTTC 2024  
Db 1713 TTGAACCTGAAAAATTTGTGCCGTTTATCATGTCTGTGAAGAAATATCGCGGTTTC 1772  
QY 2025 CTTACCAACACTGGAAGATGATGATCAGGTGGGACATCTGCATGTATTCCTTCAAA 2084  
Db 1773 CTTACCAACACTGGAAGATGATGATCAGGTGGGACATCTGCATGTATTCCTTCAAA 1832  
QY 2085 ACAACATGAGCCTCTTCCAGACCTCGAGCCAAAGCCTGTAAATTCGTGTGTGCC 2144  
Db 1833 ACAACATGAGCCTCTTCCAGACCTCGAGCCAAAGCCTGTAAATTCGTGTGTGCC 1892  
QY 2145 ATGACCTTGAGACCAAGGGGCTTCAAGTAACAGCTACCTGCAAGATTGACACCCCTGG 2204  
Db 1893 ATGACCTTGAGACCAAGGGGCTTCAAGTAACAGCTACCTGCAAGATTGACACCCCTGG 1952  
QY 2205 CGGCGCTGTATCTCCACCTTCCACATGAGGAAACAACTTCTCCAGACGCTGTCCATCC 2264  
Db 1953 CGGCGCTGTATCTCCACCTTCCACATGAGGAAACAACTTCTCCAGACGCTGTCCATCC 2012  
QY 2265 TTCAAGCTGAAGGGGCAATATCTTCTCCACCTGAGCTCAGAGGATACAGAGAGTGC 2324  
Db 2013 TTCAAGCTGAAGGGGCAATATCTTCTCCACCTGAGCTCAGAGGATACAGAGAGTGC 2072  
QY 2325 TGAAGATCATCCGAAAGCCATCATGCGCACGACCTTGCCTTATCTTTGGGAAACAGGA 2384  
Db 2073 TGAAGATCATCCGAAAGCCATCATGCGCACGACCTTGCCTTATCTTTGGGAAACAGGA 2132  
QY 2385 AGCAATTGGAAGAGATGTATCCAGACAGGATGCTGGAACCTTCCACAAACGATCCCATCGAG 2444  
Db 2133 AGCAATTGGAAGAGATGTATCCAGACAGGATGCTGGAACCTTCCACAAACGATCCCATCGAG 2192  
QY 2445 ACCGTGTACGCGCTGTATGATGATGCTGCTGTGATCTTTGCTCTGTGACAAATATGGC 2504  
Db 2193 ACCGTGTACGCGCTGTATGATGATGCTGCTGTGATCTTTGCTCTGTGACAAATATGGC 2252  
QY 2505 CAGTTACAAAATTTGACAGCGAATGATATATATGCAAAATTTGCGCTGAGGGGTGATGGA 2564  
Db 2253 CAGTTACAAAATTTGACAGCGAATGATATATATGCAAAATTTGCGCTGAGGGGTGATGGA 2312  
QY 2565 TGAAGAGCTGGGCAATACAGCCCATCTTCTATGATGACAGAGACAGAGGAGATGAATGCC 2624  
Db 2313 TGAAGAGCTGGGCAATACAGCCCATCTTCTATGATGACAGAGACAGAGGAGATGAATGCC 2372  
QY 2625 CTCAAGGACAGCTGGGATTTTCAATGCTGTGCAATTCCTGTCAATTCACCTTGAAGC 2684  
Db 2373 CTCAAGGACAGCTGGGATTTTCAATGCTGTGCAATTCCTGTGTATACACTTGAAGC 2432  
QY 2685 AGATCTTCCCAACCAAGAGCCTGTGTAAGGCTGAGAGGATTAACCTCAATCAGTGGG 2744  
Db 2433 AGATCTTCCCAACCAAGAGCCTGTGTAAGGCTGAGAGGATTAACCTCAATCAGTGGG 2492

[illegible]

RESULT 4  
AAA09591  
ID AAA09591 standard: cDNA to mRNA: 3427 BP.

AC AAA09591;

DT 29-JAN-2001 (First entry)

XX	Human phosphodiesterase 10 (PDB10) nucleotide sequence SEQ ID 3-
DE	

Phosphodiesterase 10; PDE10; human; 88.

Query Match	Beat Local Similarity	80.8%	Score 2912.4	DB 3	Length 3427	
Matches 3153	Conservative	0	Mismatches 226	Indels 35	Gaps 7	
XX Homo sapiens.						
XX OS						
XX PN JP200024992-A.						
XX PD 15-AUG-2000.						
XX PP 11-MAY-1999; 99JP-00129343.						
XX PR 30-NOV-1998; 98JP-00338861.						
XX PA (TANA ) TANABE SEIYAKU CO.						
XX WP; 2000-605129/58.						
XX Novel phosphodiesterase and its gene for research on complex mechanism of intracellular information transfer.						
XX Claim 2; Page 20-24; 29pp; Japanese.						
XX Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDB10)						
XX proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful						
XX for research on the complex mechanism of intracellular information						
XX transfer. The invention includes a recombinant vector containing a PDB10						
XX gene, and a cell transformed with the vector. Sequences AAA09593-A09606						
XX represent PCR primers used in the isolation of the PDB10 polynucleotide						
XX sequences of the invention						
XX Sequence 3427 BP; 835 A; 953 C; 892 G; 747 T; 0 U; 0 Other;						
QY Query Match	80.8%	Score 2912.4	DB 3	Length 3427		
DB Beat Local Similarity	92.4%	Pred. No. 0				
QY Matches 3153	Conservative	0	Mismatches 226	Indels 35	Gaps 7	
DB 189 GTGGGAGGGGGGGGGGGGGGGGGGGCTTCTCTGCGCTGCGATTCAGGCTTGGCTGCTCC						248
QY 12 GAGGAGAGGGGGGGGGGGGGGGGGGGCTTCTCTTGGCTGCGATTCAGGCTTGGCTGCTCC						71
QY 249 CTGCCCCGGGGGGGGGGGGGGGGGGCTTCTCCGGCCGGCTTCTCCCTACACCCGGGGTGCAC						308
DB 72 CAGCCCGCTCCGGGGGGGGGGGGGGGGGGCTTCTCCGGCCGGCTTCTCCCTACACCCGGGGTGCAC						131
QY 309 GCGCGGGGAGCTCTCGGATTTTCCGGGGGGGGGGGGGGGGGGCTTCTCCGGCCGGCTTCCGGCCGG						368
DB 132 ACCGGGCGGAGCTCTTGGGTTTTCGGGGGGGGGGGGGGGGGGCTTCTCCGGCCGGCTTCCGGCCGG						191
QY 369 GCTCTGCGGGGGGGGGGGGGGGGGGGCTTCTCCGGGGGGGGGGGGGGGGGGCTTCTCCGGGGGGGG						428
DB 192 GCTCTGCGGGGGGGGGGGGGGGGGGGCTTCTCCGGGGGGGGGGGGGGGGGGCTTCTCCGGGGGGGG						251
QY 429 CGGTTTGGCGCTGCTCTTCCGGCTTCCGATGGAAGATGGAACCTCTTAACATATGGAATT						488
DB 252 CTGCTGGCGCTGCTCTTCCGGCTTCCGATGGAAGATGGAACCTCTTAACATATGGAATT						311
QY 489 GCTTCCGAAGGCTGACCGAGTGTCTTCTCAAGCCCGAGTTTACCGATGGAAGGTTGAAGG						548
DB 312 GCTTCCGAAGGCTGACCGAGTGTCTTCTCAAGCCCGAGTTTACCGATGGAAGGTTGAAGG						371
QY 549 CCTATCTTTCTCTCCATCCCGAGTATTAAGATGAATTTGTTCTGAAGTGTTAAGTGAAG						608
DB 372 CCTATCTTTCTCTCCATCCCGAGTATTAAGATGAATTTGTTCTGAAGTGTTAAGTGAAG						431
QY 609 AGATCTGTGAAAAGTGGCTGAAGAGAAAACCAACAAAGCAAAAGATGAACCATCTCCA						668
DB 432 AGATCTGTGAAAAGTGGCTGAAGAGAAAACCAACAAAGCAAAAGATGAACCATCTCTTA						491
QY 669 AGAAGTCAAGCATACAGATACGAATATGCAAGGAGTGTGTACAGACTGAACAGCT						728
DB 492 AGAAGTCAAGCATACAGATACGAATATGCAAGGAGTGTGTACAGACTGAACAGCT						551
QY 729 ACATAGAGCAGCGCTGGAACAGGGGGGGGACACCTGCTCTCTTATGAGCTACAGA						788
DB 552 ACATAGAGCAGCGCTGGAACAGGGGGGGGACACCTGCTCTCTTATGAGCTACAGA						611

QY 789 GCATCATCAGATAGGCAAAAGCCGAGATTTCAGCTGTACTTCTTGGAGAGTGA 848  
| | | | |  
DB 612 GATATCATAGGATAGCCAAAGCCGATTTGCACTGTACTTCTTGGAGAGTGA 671  
| | | | |  
QY 849 AATAATAGCTGTGTGTGTTCAATACCACTGGGATGAAAGGCAACCCCGCTCATCC 908  
| | | | |  
DB 672 AATAATAGCTGTGTGTGTTCAATACCACTGGGATGAAAGGTCMAACCCCGCTCATCC 731  
| | | | |  
QY 909 CTGCAAGGCGCCATCAACCCAGGGTACCACTCTGTGCTTAAGTGTGCAAGTCTAAGAA 968  
| | | | |  
DB 732 CGCAGGGGCCATCAACCCAGGGCAACCACTCTGTGCTTAAGTGTGCAAGTCTAAGAA 791  
| | | | |  
QY 969 CGTTGGTGTAGAGGATATCTTGGGGATGAGCGATTTTCGAGGTATCTGGCTTGAAT 1028  
| | | | |  
DB 792 CCTGTGTGTAGAGGATATCTTGGGGATGAGCGATTTTCGAGGGCACTGGCTTGAAT 851  
| | | | |  
QY 1039 CAGGAACCCGATCCAGTCTGTCTTGTGCTTCCCATTTGCACTGCAATTGGAAGTCTTGA 1088  
| | | | |  
DB 852 CAGGAACCCGATCCAGTCTGTCTTGTGCTTCCCATTTGCACTGCAATTGGAAGTCTTGA 911  
| | | | |  
QY 1089 TTGGCAATCTTGAATCTGTAACAGGCACTGGGGCAAAAGGCTTTTGCTTCAAGCTCAAG 1148  
| | | | |  
DB 912 TTGGCAATCTTGAATCTGTAACAGGCACTGGGGCAAAAGGCTTTTGCTTCAAGCTCAAG 971  
| | | | |  
QY 1149 AGTTGCAACAGCCAACTTGTGCTTGGGCTTCCGTAGCAATACACAGGTGAGGTGTGA 1208  
| | | | |  
DB 972 AGTTGCAACAGCCAACTTGTGCTTGGGCTTCCGTAGCAATACACAGGTGAGGTGTGA 1031  
| | | | |  
QY 1209 GAGGTCGTGCGCAACAGACCGAATGATGACTTCTTCTGATCGATCAAGCAATCACT 1268  
| | | | |  
DB 1032 GAGGTCGTGCGCAACAGACCGAATGATGACTTCTTCTGATCGATCAAGCAATCACT 1091  
| | | | |  
QY 1269 TTGATTAACATACTTGGCATAGACTCTCTACTTGAACATCATGATATATGAAAAATC 1328  
| | | | |  
DB 1092 TTGATTAACATACTTGGCATAGACTCTCTACTTGAACATCATGATATATGAAAAATC 1151  
| | | | |  
QY 1339 TAGTGAACGCGACCGCTGCGGCTCTTCAAGTGAACCAAGAACAGAGCTGTACT 1388  
| | | | |  
DB 1152 TAGTGAACGCGACCGCTGCGGCTCTTCAAGTGAACCAAGAACAGAGCTGTACT 1211  
| | | | |  
QY 1389 CGGACTGTGTTGACATTTGGGAGAGAAAGAGGAGGCCCATCTTCAAGAAACCAAG 1448  
| | | | |  
DB 1212 CGGACTGTGTTGACATTTGGGAGAGAAAGAGGAGGCCCGCTTCAAGAAACCAAG 1271  
| | | | |  
QY 1449 AGATCAGATTTTCCATTGAAAGGAGTTGCTGTCAATGTGCAAGAACAGGCAAGTCT 1508  
| | | | |  
DB 1272 AGATCAGATTTTCCATTGAAAGGAGTTGCTGTCAATGTGCAAGAACAGGCAAGTCT 1331  
| | | | |  
QY 1509 TGAACATTTCCGATGCTACGCGGACCCCTCGCTTTAAACAGGAGGTGACCTGTACAG 1568  
| | | | |  
DB 1332 TGAACATTTCTGATGCTACGCGAGCCGCGCTTTAAACAGGAGGTGACCTGTACAG 1391  
| | | | |  
QY 1569 GCTACACCAAGAGAACTTCTGTGTATGCCCATAGTGAAGCCGAGCAGCTGTATTTGCG 1628  
| | | | |  
DB 1392 GCTATACCAAGAGAACTTCTGTGTATGCCCATAGTGAAGCCGAGCAGCTGTATTTGCG 1451  
| | | | |  
QY 1629 TGTGTGAGTGTGTAAACAAGATCAGCGGTAGCGCTTCTTCAAGACAGAGAACTT 1688  
| | | | |  
DB 1452 TGTGTGAGTGTGTAAACAAGATCAGCGGTAGCGCTTCTTCAAGACAGAGAACTT 1511  
| | | | |  
QY 1689 TCAAGATGTTTGTCTGTCTGTGCGACCTGTGCGCTTGTGCTTAACATGTACACAGA 1748  
| | | | |  
DB 1512 TCAAGATGTTTGTCTGTCTGTGCGCTGTGCGCTTGTGCTTAACATGTACACAGA 1571  
| | | | |  
QY 1749 TCCGCACTCAGAAATCTTACAGGGTTACCATGAGAGAGCTTTCTTACACAGACTCT 1808  
| | | | |  
DB 1572 TCCGCACTCAGAAATCTTACAGGGTTACCATGAGAGAGCTTTCTTACACAGACTCT 1631  
| | | | |  
QY 1809 GCACTCTCGAGAGTGTGCAAGGCTCTTCACTGCTTCAACAGACGCACTGTGCGGG 1868  
| | | | |  
DB 1632 GCACTCTCGAGAGTGTGCAAGGCTCTTCACTGCTTCAACAGACGCACTGTGCGGG 1691  
| | | | |

QY 1869 ACATGAGACTATTCACCTTGAATTTGATGATTTGCTTTGAGAAATGTGGCTGGGATCTTTG 1928  
| | | | |  
DB 1692 ACATGAGACTATTCACCTTGAATTTGATGATTTGCTTTGAGAAATGTGGCTGGGATCTTTG 1751  
| | | | |  
QY 1929 TCTACATGATCCATGTGTCTTGTGGGACATCTGTTTTGAACCTTGAATAATGTGCCGT 1988  
| | | | |  
DB 1752 TCTACATGATCCATGTGTCTTGTGGGACATCTGTTTTGAACCTTGAATAATGTGCCGT 1811  
| | | | |  
QY 1989 TTATCATGCTGTGAAAGAACTATCGGCGGCTTCTTACCAACAACCTGGAAGATGACG 2048  
| | | | |  
DB 1812 TTATCATGCTGTGAAAGAACTATAGCGGGTTCTTACCAACAACCTGGAAGATGACG 1871  
| | | | |  
QY 2049 TCACGATGCAACATGATATGCAATCTTCAAAACAACAATGAGCTTTCAAGAAC 2108  
| | | | |  
DB 1872 TCACGATGCAACATGATATGCAATCTTCAAAACAACAATGAGCTTTCAAGAAC 1931  
| | | | |  
QY 2109 TCGAGCGCAAGGCTGCTTAATTTGCTGTCTGTGCAATGACCTTGAACCAAGGGCTTCA 2168  
| | | | |  
DB 1932 TCGAGCGCAAGGCTGCTTAATTTGCTGTCTGTGCAATGACCTTGAACCAAGGGCTTCA 1991  
| | | | |  
QY 2169 GTAAAGCTACCTGCAAGAGTTGACCAACCCCTGAGCGGCTGTACTTCACTTCAACCA 2228  
| | | | |  
DB 1992 GTAAAGCTACCTGCAAGAGTTGACCAACCCCTGAGCGGCTGTACTTCACTTCAACCA 2051  
| | | | |  
QY 2239 TGGAGCAACACCACTTCTCCAGAGGATGTCATCTTCAAGTGAAGGGCACAATATCT 2288  
| | | | |  
DB 2052 TGGAGCAACACCACTTCTCCAGAGGATGTCATCTTCAAGTGAAGGGCACAATATCT 2111  
| | | | |  
QY 2289 TTTCCACCTGAGCTTCCAGAGTACAGAGTACAGAGTGTGATCATCTGGCAAGGCATCA 2348  
| | | | |  
DB 2112 TTTCCACCTGAGCTTCCAGAGTACAGAGTACAGAGTGTGATCATCTGGCAAGGCATCA 2171  
| | | | |  
QY 2349 TCGCACCGACCTGCGCCTATATCTTTGGGAAACAGGAACAAGTGAAGAGATGTACAGA 2408  
| | | | |  
DB 2172 TCGCACCGACCTGCGCCTATATCTTTGGGAAACAGGAACAAGTGAAGAGATGTACAGA 2231  
| | | | |  
QY 2409 CAGGCTGCTGCAACCTTCAACAACAGTCCATTCAGACCGGTGTCATCGGCTTGTATGTA 2468  
| | | | |  
DB 2232 CAGGCTGCTGCAACCTTCAACAACAGTCCATTCAGACCGGTGTCATCGGCTTGTATGTA 2291  
| | | | |  
QY 2469 CTGCTGTGATCTTTGCTGTGTACCAAACTATGCGCGATTACAAATTTGACAGGAAATG 2528  
| | | | |  
DB 2232 CTGCTGTGATCTTTGCTGTGTGTGCAAGAACTATGCGCGATTACAAATTTGACAGGAAATG 2351  
| | | | |  
QY 2529 AATATATGCAGAATTTGCGGCTGAGGGTGAATGATGAAGAAGCTGGGCAATACAGCCA 2588  
| | | | |  
DB 2352 AATATATGCAGAATTTGCGGCTGAGGGGATGAATGAAGAAGTTGGGATACAGCCA 2411  
| | | | |  
QY 2589 TTCTATGATGACAGAGACAGACAGAGTGAAGTCCCTCAAGGGCAAGCTCGGATTTTCA 2648  
| | | | |  
DB 2412 TTCTATGATGACAGAGACAGAGACAGAGTGAAGTCCCTCAAGGACAGCTTGTGATTTCA 2471  
| | | | |  
QY 2649 ATGCTGTGCAATTTCTGTCTATACACCTTGAACGCAATCTTCCACCAAGAGCTTC 2708  
| | | | |  
DB 2472 ATGCTGTGCAATTTCTGTCTATACACCTTGAACGCAATCTTCCACCAAGAGCTTC 2531  
| | | | |  
QY 2709 TGTCTGAAGGCTGCGAGGATTAACCTCAATCAAGTGGGAAGAGGTAATTTGCGGGGAAGA 2768  
| | | | |  
DB 2532 TGTCTGAAGGCTGCGAGGATTAACCTCAATCAAGTGGGAAGAGGTAATTTGAGGGGAAGA 2591  
| | | | |  
QY 2769 CAGCAATGTGATTTCAAGGCCCAAGGCCCGCGCTTGAAGAGCAACCTGAGAGTGA 2828  
| | | | |  
DB 2592 CAGCAATGTGATTTCAAGGCCCA-----GCAACTGAGCAAAAGCAACTGTGAGAGCCGA 2645  
| | | | |  
QY 2829 ACGTGAAGTTGAAGATGTATCTGAAGTGAACGTCTGTATGTCTGCGCAACCGACTC 2888  
| | | | |  
DB 2646 CAGCAAGTGTGATGTATCTGAAGTGAACGTCTGTATGTCTGCGCAACCGACTC 2697  
| | | | |  
QY 2889 AACCTGCTTGTGATCTTGTCTTT-----TGTTTCAAGGGGGAAGAAACCCCT 2940  
| | | | |  
DB 2698 AACCTGCTTGTGATCTTGTCTTTTATTTTATTTTATTTTAAACGGGGTGAAGAACTCT 2757  
| | | | |  
QY 2941 GTCAAGAGTACCGTGCATATCCATGTGAAGACAGACTCCCTGCTTGGCGCACAGC 3000  
| | | | |

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Db      2758 CTGAGAGGTACCGTGCATATCCATGTAGAGAGTGAATCTCTCT-----GCGCACAC 2810
Qy      3001 CTGAGACATGAGCAACCCAGGCTGCGGTGTTTCAGAGCGTGGCTACTCCGTGCTCCA 3060
Db      2811 CTGAGACCTGAGCAACCCGGGCTCCACCGTGTTCAGAGCGTGGCTACTTCATGCTCCG 2870
Qy      3061 CCTGACCTCCGAATGCTATTGTGCTCCAGGCGCAGCACTGCACTGTCTGAGGGGGCAGAG 3120
Db      2871 CTGAGACCCCGAATGCTATTGTGCTACAGGCGCAGAACTGCGCTGGAGGGGGCAGAG 2930
Qy      3121 ACCACGAGAGAGGTTTGTGCTGCTCATCTCCCACTGAGGGGTGGG---CCAGTCCCTGGT 3177
Db      2931 ACGACGAGAGGGGTTCTTACCTGCAATCTTCATGAGGGGTGGTCTGTGTTCAATCTC 2990
Qy      3178 TCTGTGTCATGCTGCTGCTGTGTCATGTTAGTAAGTAAGGACACAGCCCTGTGTGT 3237
Db      2991 TTAACAGAGATGCTACTGCTGTGCTGGCGTTGTGTTAGAAATGGACACATGCCCC-TGTGCT 3049
Qy      3238 GAAATTACATGATGACCTTCTTAAAGGTTAACTGAGTTGTGTGCTGGGACACATGTAAT 3297
Db      3050 GAAATTACATGATGACCTTCTTAAAGGTTAACTGAGTTGTGTGCTGGGACCTCTGTAAT 3109
Qy      3298 GAAAGTCAAGTGTCAAGGTGAGAGAGAAATCCAACTGTGTTAAAGGTGACTACAG 3357
Db      3110 GAAAGTTCAGTGCACAGGTGATAGAAATTTCAAGCTGTAACTACAGGTGACTACAA 3169
Qy      3358 GTATGCTCTTTCAGTCTATCTGAGGGGACATAGGTGAGTGTGCTCACTCAGAGGAAGC 3417
Db      3170 GTGTGTTCATTGATGTTTACCTGGGGGCAATGAGGTGAGTCACTCCACAGAGAAAGAAC 3229
Qy      3418 ATACCTCTGCTTCATCTCAGAGGGGACACAGGGTACATCCAGGCACTGGGAACTGAAGCT 3477
Db      3230 ATACCTCTGCTTCATCTCAGAGGGGACACAGGGTACATCCAGGCACTGAAG-- 3287
Qy      3478 CTGACTTCAAAACATGTCAAAAGAAATTAACACCTCCCTCCCTCCCTCACTGTAGCCCTTG 3537
Db      3288 CTCACCTCAAAACATGTCAAAAGAAATTAACACACCCCTCCCTCCCTCACTGTAGCCCTTG 3347
Qy      3538 GCAACTGCGCCATCCCTTATATCAAAAGAAATTAAGTAAGGCAATTAATTT 3591
Db      3348 GCAACTTCCGCAACCTTTCACACAAAGAAATTAAGTAAGGCAATTAATTT 3401

RESULT 5
ACC48919 standard; cDNA; 3219 BP.
AC  ACC48919;
XX
XX
XX  11-AUG-2003 (first entry)
DT  XX
XX
XX  Rat phosphodiesterase 10A cDNA.
DE  XX
XX
XX  Rat; phosphodiesterase 10A; PDE10A; enzyme; tranquilizer; neuroleptic;
KM  mootropic; antiaddictive; gene; ss.
XX
XX  Rattus sp.
OS
XX
XX  Key      Location/Qualifiers
XX  FH      116..2440
XX  FT      /tag= a
XX  FT      /product= "PDE10A"
XX  FT      /transl_except= (pos:272..280,aa:Val-Arg)
XX  FT      /transl_except= (pos:1232..1249,aa:Gln-Val)
XX  FT      /transl_except= (pos:1904..1912,aa:Ser-Tyr)
XX  FT      /transl_except= (pos:2435..2437,aa:DVD)
XX
XX  EP1281771-A2.
XX
XX  05-FEB-2003.
XX
XX  16-JUL-2002; 2002EP-00254973.

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XX  31-JUL-2001; 2001US-0308978P.
PR
XX
XX  (PF12 ) PRIZER PROD INC.
PA
XX
XX  James LC, Lebel LA, Mennuti FS, Strick CA;
PI
XX
XX  WPI; 2003-335006/32.
DR
XX
XX  P-PSDB; ABR42040.
DR
XX
XX  Screening for agents that inhibit intracellular phosphodiesterase 10A
PT  activity for use in treating disorders of movement of mood and anxiety,
PT  by using striatal medium spiny neurons to identify inhibitors at cellular
PT  level.
XX
XX  Claim 10; Fig 1A; 27pp; English.
XX
XX  The present sequence is that of cDNA encoding rat phosphodiesterase 10A
CC  (PDE10A). Human PDE10A was used to screen an expressed sequence tag (EST)
CC  database, and a rat EST having homology to an internal portion of the
CC  human protein was identified. EST and RACE information identified the 5'
CC  and 3' ends of the sequence from rat brain RNA, and the present full-
CC  length rat PDE10A cDNA was obtained by PCR amplification. The invention
CC  provides a cell-based assay using striatal medium spiny neurons to
CC  identify agents that inhibit PDE10A activity at the cellular level. The
CC  inhibitors are useful e.g. for treating disorders of movement or mood,
CC  anxiety, psychosis, drug addiction, and disorders of symptom deficient
CC  cognition
XX
XX  Sequence 3219 BP; 849 A; 836 C; 829 G; 705 T; 0 U; 0 Other;
SQ
XX
XX  Query Match      72.4%; Score 2610.6; DB 10; Length 3219;
XX  Best Local Similarity 91.9%; Pred. No. 0;
XX  Matches 2844; Conservative 0; Mismatches 214; Indels 35; Gaps 7;
XX
Qy      525 GTTTCAGGATGAAAGGTGAAGGCTATCTTCTCCATCCCGAGTATTAGATGAAT 584
Db      123 GTTTCAGGATGAAAGGTGAAGGCTATCTTCTCCATCCCGAGTATTAGATGAAT 182
Qy      585 TTGTTCTGAAAGTGTAACTGACAGACCTGTGAAAAGTGGCTGAAGAGAAACCAACA 644
Db      183 TTGTTCTGAAAGTGTAACTGACAGACCTGTGAAAAGTGGCTGAAGAGAAACCAACA 242
Qy      645 AAGCAAAAGATGAACATCTCCCAAGAGTCAAGAGGTACAGAGTAAAGATATGACAG 704
Db      243 AAGCAAAAGATGAACATCTCCCAAGAGTCAAGAGGTACAGAGTAAAGATATGACAG 302
Qy      705 GAGTGTATACGAGCTGAACAGCTACATAGAGCGGCTTGACACAGGCGGGGACAAC 764
Db      303 GAGTGTATACGAGCTGAACAGCTACATAGAGCGGCTTGACACAGGCGGGGACAAC 362
Qy      765 ACCTGCTCTCTATAGACTCAGACGATCATCAGATAGCCACAAAGCCGACGATTTG 824
Db      363 ACCTGCTCTCTATAGACTCAGACGATCATCAGATAGCCACAAAGCCGACGATTTG 422
Qy      825 CACTGTACTTCTTGAAGAGTGAATATAGCTGTGTGTGTTCAATACACCCGGGATGA 884
Db      423 CACTGTACTTCTTGAAGAGTGAATATAGCTGTGTGTGTTCAATACACCCGGGATGA 482
Qy      885 AGGAAGGCCAACCCGGGCTCATCCCTGACAGGCGCCATCAACCCAGGGTACCAACCATCTG 944
Db      483 AGGAAGGTCAACCCCGCTCATCCCGACAGGCGCCATCAACCCAGGGTACCAACCATCTG 542
Qy      945 CTTACGTGGCCAAGTCTAGAAAGCTGTGTGTAGAGATATCTTGGAGTAGAGCAT 1004
Db      543 CTTATGTGGCCAAGTCTAGAAAGCTGTGTGTAGAGATATCTTGGAGTAGAGCAT 602
Qy      1005 TTCTTGAGGTACTGCTGCGCTGGAATCAGAAACCGGATCCAGTGTGTTCTTTCGCCCA 1064
Db      603 TTCCAGAGGCACTGTGTGAGATCAGAAACCGGATCCAGTGTGTTCTTTCGCCCA 662
Qy      1065 TTGTCACTGCAATGAGACTTGAATGGCACTTGAATGTACAGAGCACTGGGCAAG 1124

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Db 663 TTGTGACTGGCATTTGGAGCTTGAATTGGACCTTGAAGGCACTGGGGGAAAG 722  
Oy 1125 AGGCTTTGCTTCAAGCCATCAGAGGTTTGCAAGCCAACTTGTGGCTTCCGTAG 1184  
Db 723 AGGCTTTGCTTCAAGCCATCAGAGGTTTGCAAGCCAACTTGTGGCTTCCGTAG 782  
Oy 1185 CAATACACAGGTTGAGGTTGAGAGGCTGCGCCAAACAGACCGAATGAATGAATTCC 1244  
Db 783 CAATACACAGGTTGAGGTTGAGAGGCTGCGCCAAACAGACCGAATGAATGAATTCC 842  
Oy 1245 TACTGACGTATCAAGAATATCTTGTATACATAGTTGCCATAGACTCTACTTGAAC 1304  
Db 843 TGCTGATGATCAAGAATATCTTGTATACATAGTTGCCATAGACTCTACTTGAAC 902  
Oy 1305 ACATCATGATATATGCAAAAAATCTAGTGAAGCCGACCGCTGCGGCTCTTCCAGTGG 1364  
Db 903 ACATCATGATATATGCAAAAAATCTAGTGAAGCCGACCGCTGCGGCTCTTCCAGTGG 962  
Oy 1365 ACCAAGAAGCAAGAGGCTGTCTGGAACCTGTTGACATTTGGGGAGAGAGGGGA 1424  
Db 963 ACCAAGAAGCAAGAGGCTGTCTGGAACCTGTTGACATTTGGGGAGAGAGGGGA 1022  
Oy 1425 AGCCCATCTTCAAGAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTC 1484  
Db 1023 AGCCCATCTTCAAGAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTC 1082  
Oy 1485 AAGTGGCAAGAACAGGCGAAGTTCTTGAACATTTCCGATGCTTACGCGGACCTCGCTTA 1544  
Db 1083 AAGTGGCAAGAACAGGCGAAGTTCTTGAACATTTCCGATGCTTACGCGGACCTCGCTTA 1142  
Oy 1545 ACAGGAGGTGAGCTGTACACAGGCTACACAGAGAGAACTTGTGTATGGCCATAG 1604  
Db 1143 ACAGGAGGTGAGCTGTACACAGGCTATACACAGGAGAACTTGTGTATGGCCATAG 1202  
Oy 1605 TGAGCGAGGCAAGCTGTATGAGCTGTGTCAGATGCTGAACAAGATCAGCGGTAGCGCT 1664  
Db 1203 TGAGCGAGGCAAGCTGTATGAGCTGTGTCAGATGCTGAACAAGATCAGCGGTAGCGCT 1262  
Oy 1665 TCTCCAAAGACAGAGAACTTCAAGATGTTTGTCTCTTCTGCGGACCTGGCTTGC 1724  
Db 1263 TCTCCAAAGACAGATAGAACTTCAAGATGTTTGTCTCTTCTGCGGCTGGCTTGC 1322  
Oy 1725 ACTGTCATACATGTACCAAGAGATCCGCACTCAGAAATGATCTACAGGGTTACATAG 1784  
Db 1323 ACTGTCATACATGTACCAAGAGATCCGCACTCAGAGTGCATACAGGGTTACATAG 1382  
Oy 1785 AGAAGCTTCTTACCAAGCATCTGCACTCCAGAGAGTGGCAGAGCCTCATGCGCTTCA 1844  
Db 1383 AGAAGCTGCTTACCAAGCATCTGCACTCCAGAGAGTGGCAGAGCCTCATGCACTTCA 1442  
Oy 1845 ACTTACAGAGCATCTGCGCGGAGCATGAGACTTTCATCTTGAATTTGCTCTTTCG 1904  
Db 1443 ACTTCCAGAGCATCTGCGCGGAGCATGAGACTTTCATCTTGAATTTGCTCTTTCG 1502  
Oy 1905 AGAATATGAGCTGTGGATCTTGTCTACATGATCATGATCTGTGGGACATCTGTT 1964  
Db 1503 AGAATATGAGCTGTGGATCTTGTCTACATGATCATGATCTGTGGGACATCTGTT 1562  
Oy 1965 TTGAATTTGAAAAATTTGTCGCTTTTATCATGTCTGTGAAGAACTATCGCGGGTTC 2024  
Db 1563 TTGAATTTGAAAAATTTGTCGCTTTTATCATGTCTGTGAAGAACTATAGCGGGTTC 1622  
Oy 2025 CTTACCAAGCTGGAAGCATGAGTCAAGGTGGCACTGCACTGTATGTCATTTCAAA 2084  
Db 1623 CTTACCAAGCTGGAAGCATGAGTCAAGGTGGCACTGCACTGTATGTCATTTCAAA 1682  
Oy 2085 ACAAAATGAGCTCTTCAAGAGCTCGAGCGCAAGAGGCTGCTATTTGGGTCTGTGTC 2144  
Db 1683 ACAAAATGAGCTCTTCAAGAGCTTGAAGCGCAAGGCTGCTATTTGGGTCTGTGTC 1742  
Oy 2145 ATGACCTGGAACCAAGGGCTTCAAGTAAAGCTTACCTGCAAGAGTTGCAACCCCTGAG 2204  
Db 1743 ATGACCTGGAACCAAGGGCTTCAAGTAAAGCTTACCTGCAAGAGTTGCAACCCCTGAG 1802

Oy 2205 CGGCGCTGTATCTCAACCTCCACCAATGAGGAAACACCACTTCCCGAGCGGTCATCC 2264  
Db 1803 CTGCGTGTATCTCAACCTCCACCAATGAGGAAACACCACTTCCCGAGCGGTCATCC 1862  
Oy 2265 TTCACTGGAAGGAGCAATATCTTCTCACCTGAGCTCCAGCGAGTACAGAGAGTGC 2324  
Db 1863 TTCACTGGAAGGAGCAATATCTTCTCACCTGAGCTCCAGCGAGTACAGAGAGTGC 1922  
Oy 2325 TGGAGATCATCCGCAAGCAGCATATCCGCAAGAGCTGCGCTTATCTTTGGGAAACAGA 2384  
Db 1923 TGGAGATCATCCGCAAGCAGCATATCCGCAAGAGCTGCGCTTATCTTTGGGAAACAGA 1982  
Oy 2385 AGCAGTTGAGAGAGTGTACCAAGAGAGGAGTGGTGAACCTCCACAAAGAGTCCATGAG 2444  
Db 1983 AGCAGTTGAGAGAGTGTACCAAGAGAGGAGTGGTGAACCTCCACAAAGAGTCCATGAG 2042  
Oy 2445 ACCGTGTATCGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2504  
Db 2043 ACCGTGTATCGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102  
Oy 2505 CAGTTACAAAATTGACAGCGAATGATATATGCAAAATTCTGGCTGAGGCTGATGAGA 2564  
Db 2103 CAGTTACAAAATTGACAGCAATGATATATGCAAGTCTGGGCTGAGGGGATGAGA 2162  
Oy 2565 TGAAGAAGCTGGGCAATACAGGCTATCTATGATGAGAGAGAGAGAGAGAGAGAGAGAG 2624  
Db 2163 TGAAGAAGCTGGGCAATACAGGCTATCTATGATGAGAGAGAGAGAGAGAGAGAGAGAG 2222  
Oy 2625 CTCAAGGAGCTCGGATTTCAATGCTGTGAGCCATTCCTGCTATACCACTTGAAGC 2684  
Db 2223 CTCAAGGAGCTCGGATTTCAATGCTGTGAGCCATTCCTGCTATACCACTTGAAGC 2282  
Oy 2685 AGATCTTCCACCCACAGAGCTCTGCTGAAGGCTGCAAGGATTAACCTCAATCAGTGG 2744  
Db 2283 AGATCTTCCACCCACAGAGCTCTGCTGAAGGCTGCAAGGATTAACCTCAATCAGTGG 2342  
Oy 2745 AGAAGTAAATTCGCGGGGAG 2804  
Db 2343 AGAAGTAAATTCGAGGGAG 2396  
Oy 2805 GCAAGAGCAACTGAGAGAGCTGAACCTGAAGGTTGAAGCTGATCTGAAGTGAAGTCC 2864  
Db 2397 GCAAGAGCAACTGAGAGAGCTGAACCTGAAGGTTGAAGCTGATCTGAAGTGAAGTCC 2448  
Oy 2865 TGATGTCTGCGCAGAGCAAGCACTCACTGCTGTGTGATCTTCTTTTGG----- 2917  
Db 2449 TGATGTCTGCGCAGAGCAAGCACTCACTGCTGTGTGATCTTCTTTTATTTTAT 2508  
Oy 2918 -TTTTCAGAGGGGTGAAGACCCCTGTGAGAGGTACCGTGGCATATCCATGTAAGAGAGA 2976  
Db 2509 TTTTTCAGAGGGGTGAAGACCCCTGTGAGAGGTACCGTGGCATATCCATGTAAGAGAGA 2568  
Oy 2977 GCACTCCCTGCTTGGCCGACACACTCGAGACAGTGAAGCAACCAAGCTCTGCGGTGTTCA 3036  
Db 2569 GCACTCCCT-----GGGACACCTGGGACCGTGAAGCAACCGGGCTTCCACCGTGTCA 2621  
Oy 3037 GACGTGCGCTACTCCGTGGCTCACCTTGAACCTCGAATGTATTTTGTCCAGGCGACGA 3096  
Db 2622 GACATCGGCTATTTCCATGTGCTCCGCTGACCCCGAAGCCATTTGCTACAGAGGCAAGA 2681  
Oy 3097 CTGCACTGTCTGGAAGGGGAGAGAGCAAGAGAGGTTCTTGGCTGATCTCCCATGA 3156  
Db 2682 CTGCGCTGAGAGGGGAGAGAGAGAGAGAGGAGGTTCTTACCTGATCTTTCATGA 2741  
Oy 3157 GGGTGTGG---CAATTCCTGTGTGTGTCATGCTGCTGCTGTGGGCAATGTTAGG 3213  
Db 2742 GGGT 2801  
Oy 3214 AATGGAGACACAGCCCTTGTGTGAAATTTATCATGTGAACCTTCTTATAGTTAACTGAG 3273  
Db 2802 AATGGAGACACAGCCCT--TGTGTGAAGTTTATCATGTGAACCTTCTTATAGTTAACTGAG 2860



QY	3374	TTTGTGGCTTGGGACACATGTAATGAAGTCAACAGTCCACAGGTGACAGAAATCCAA	3333
Db	2861	TTCCTAGCTGGGACCCCTGTAAAGAGTTACAGTCCACAGGTGATGAAGAAATCCAG	2920
QY	3334	CTGTGATTACAGGTGACTACAGGTATGCTCTTTCACTATCTTGSGGGACATAGGTG	3393
Db	2921	CTGTAAGTACAGGTGACTATAACTGTGTTCACTTCACTTTACTGGGGCATGAGGTG	2980
QY	3394	AGTCTGCTCACTCAGAAAGAAAGACTACCTCTGCCCCATCCAGGGACACAGGTACAT	3453
Db	2981	AGTCAGCTCCACAGAGAAAGAAAGACTACCTCTGCCCTCATCAAGGGACACAGGTACAT	3040
QY	3454	CCCAAGGACATGSGGAACTGAAGCTCTCACTTCAAAACAATGTCAAAAGATTAAACACTC	3513
Db	3041	CCCAAGGACATCAGAGAACTGCAG--CTCACTTCAAAACAATGTCAAAAGATTAAACACACC	3098
QY	3514	CCCTTCCCCCTCACTGTACCTTTGGGCACTGGCCCAATCCCTTTATCAAAAGAAATAA	3572
Db	3099	CCCATTCCTCTCACTGTACCTTTGGGCACTTGGCCCAACCTTCAACAAAGAAATAA	3158
QY	3574	AGTAAGCATTAATTTAAAAAATAAAAAA	3606
Db	3159	AGTAAGCGTATAAATTTCTTCACAGAAACAA	3191

RESULT 6  
AAZ47000  
ID AAZ47000 standard; DNA; 4076 BP.

DT 05-JUN-2000 (first entry)

Rat phosphodiesterase encoding genomic DNA.

KW Phosphodiesterase; rat; brain, cellular response; hormone; neurotransmitter; ds.

OS Ratus sp.

Key	Location/Qualifiers
FH	

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PT      /tag= a
PT      /product= "phosphodiesterase"

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PN EP980911-A2.

PD 23-FEB-2000.

04-JUN-1998; 98EP-00110192.

04-JUN-1998; 98BP-00110192.

PA (FARB ) BAYER AG.

PI Wunder F;

WPI: 2000-258589/23

DR E-PSDB; AA13/306.  
XX

cellular response to hormones and neurotransmitters.

xx  
PS  
Claim 1: Fld 1: 13pp: English.

This DNA encodes a phosphodiesterase, derived from rat brain.

CC Phosphodiesterases are regulators of the cellular response to c.g.  
CC hormones and neurotransmitters

Sequence 4076 BP: 1040 A: 1044 C: 1039 G: 953 T: 0 U: 0 Other:

Query Match 69.3%; Score 2498; DB 3; Length 4076;

Best Local Similarity 91.9%; Pred. No. 0;

Matches 2726; Conservative 0; Mismatches 205; Indels 35; Gaps 7;

QY	652	AGATGAAACAATCTCCCAAGAGATCGACAGGTACCAAGATACAAATATGCAAGAAATCGT	711
Db	1129	AGATGAACCAATCTCTTAAGGAATCTACAGAGGTACCAAGAACCAATGCAAGGAATCGT	1188
QY	712	GTAAGACTGAACAAGCTACATAGAGCAGCGCTTGGAACAGGGGGGGGACAAACAACCTGCT	771
Db	1189	GTAACAGCTTAAAGAGCTACATAGAGCAGCGCTTGGAACAGGGGGGGGACAAACAACCTGCT	1248
QY	772	CTCTATAGACTCAGCAGCATCATCAGATAGGCACAAAGCCGACGGAATTTGCACTGTA	831
Db	1249	CTGTACAGACTTAAGCATGTAATCATCAGATAGGCACAAAGCCGACGGAATTTGCACTGTA	1308
QY	832	CTTCTTGGAGAGTGCATATATATAGCTGTGTGTGTATACACCCGGGATGAAGAGG	891
Db	1309	CTTCTTGGAGAGTGCATATATATGTGTGTGTGTCTTACACCAACCCGGAATGAAGAGG	1368
QY	892	CCAAACCCCGCTATCCCTGACAGGCCCATCACCCAGAGGTACCAACATCTGTGCTACGT	951
Db	1369	TCAACCCCGCTCATCCCGCCAGGCCCATCACCCAGAGGTACCAACATCTGTGCTATGT	1428
QY	952	GGCCAACTTAAGGAAGAGTGTGTGTGTGAAGAGATCTTGTGGGATAGAGATTTCTCG	1011
Db	1429	GGCCAACTTAAGGAAGAGCTGTGTGTGTGAAGAGATCTTGTGGGATAGAGATTTCTCCAG	1488
QY	1012	AGGTACTGAGCTGGAAATCAGAGAACCCGCAATCCAATCTGTCTTTGCTTGCCCATTTGCAC	1071
Db	1489	AGGCACTGTGTGGAAGTCAAGAACCCGAATCCAATCTGTCTTTGCTTGCCCATTTGTAC	1548
QY	1072	TGCCATTGGAGACTTGAATTTGGCACTCTTGAACGTGTAAGGCACTGGGGCAAAAGAGGCTT	1131
Db	1549	TGCCATTGGAGACTTGAATTTGGCACTCTTGAACGTGTAAGGCACTGGGGCAAAAGAGGCTT	1608
QY	1132	CTGCTCAGACCATATAGAGGTTGTGACAGCCAACTTGTGGCTTCCGTAGCAATACA	1191
Db	1609	CTGCTCAGACCATATAGAGGTTGTGACAGCCAACTGTGGCTTCCGTAGCAATACA	1668
QY	1192	CCAGGTGCAAGTGTGTAGAGGTCTTGCCAAACAGACCGAACTGAATGACTTCTTACTTCTGA	1251
Db	1669	CCAGGTGCAAGTGTGTAGAGGTCTTGCCAAACAGACCGAACTGAATGACTTCTTACTTCTGA	1728
QY	1252	CGTATTCAAAGACATATCTTGAATAATATGTGCAATATGACTCTCTATCTTGAACATCAT	1311
Db	1729	TGTAATCAAAGACATATCTTGAATAATATGTGCAATATGACTCTCTATCTTGAACATCAT	1788
QY	1312	GATATATGCAAAAAATCTATGAAACGCGCAACCGCTGCGCTCTTCCAGGTGACCAAA	1371
Db	1789	GATATATGCAAAAAATCTATGAAACGCGCAACCGCTGCGCTCTTCCAGGTGACCAAA	1848
QY	1372	GAACAAGAGCTGTACTCGACCTGTTTGACATTTGGGGAGAGAAAGAGGGGAAGCCCAT	1431
Db	1849	GAACAAGAGCTGTACTCGACCTGTTTGACATTTGGGGAGAGAAAGAGGGGAAGCCCGT	1908
QY	1432	CTTCAAGAAGACAAAGAGATCAGATTTTTCATTTGAGAAAGGATGTGTGCTCAAGTGGC	1491
Db	1909	CTTCAAGAAGACAAAGAGATCAGATTTTTCATTTGAGAAAGGATGTGTGCTCAAGTGGC	1966
QY	1492	AAGAACAGGCAAGTCTTGAACATTTCCGATGCTTACGCGGACCTCGCTTTAACAGGGA	1551
Db	1969	AAGAACAGGCAAGTCTTGAACATTTCCGATGCTTACGCGGACCTCGCTTTAACAGGGA	2028
QY	1552	GGTGACCTGTACACAGGCTACACACAGAGAACATTTGTGTATAGCCCATATGTAGGCG	1611
Db	2029	GGTGACCTGTGTACAGGCTATACACACGCGGAACATTTGTGTATAGCCCATATGTAGGCG	2086
QY	1612	AGGCAAGCTGATTTGGCTGTGTGACAGATGTGTGAACAAAGATCAGCGGTACGCGCTTCCAA	1671
Db	2089	CGGCAAGCTGATTTGGCTGTGTGTGACAAATGTGTGAACAAAGATCAGCGGCAAGCGCTTCCAA	2146
QY	1672	GACAGACAGAACCAATTCAGAGATTTGTGTCTTCTTGCCGACTGCGCTTGCACCTGTGC	1733
Db	2149	GACGATAGAACCAATTCAGAGATTTGTGTCTTCTTGCCGCTGTGCGCTTGCACCTGTGC	2206

[illegible]

QY	2812	CACACCTGAGAAAGCTGAAACGTGAAGGTTGAAAGATGATCCGAAAGTACAGTCCGATGTC	2871
Db	3283	CACATCTGAGAAAGCCGACCAAGAAAGGTCGATGACGTATCCCGAGG-----TGATGTC	3334
QY	2872	TGCCAGCAACCGAAGCTGAAACCTGCTCTGTGATCTTCGTTCTTTTGTGTTTC-----A	2923
Db	3335	TGCTTAGCACTGACTCAACCTGCTCTGTGATCTTCGTTCTTTTATTTTATTTTTLA	3394
QY	2924	AGGGGTGAAAAACCCCTGTCAAGAAAGTACCGTGCATATCCATGTGAAGCAGACGACTCC	2983
Db	3395	ACGGGGGTGAAAAACCTCTCTCAGAAAGTATACGTCGCATATCAATGTGAAGCAGATGACTCC	3454
QY	2984	CTGCTTGCCCGACACACTCTGGGACAGATGAGAACACCGAGGCTCTGCGGTTCACACGTCG	3043
Db	3455	CT-----GGGCACACCTCGGACCGTGAAGAACCCGGGCTCCACCGGTGTCACACGTCG	3507
QY	3044	GCTACTCCGTGGCTCCACCTGACCTGCAGAAAGTATATTTGCTCCGAGGACAGACGTGCACT	3103
Db	3508	GCTATTTCCATGAGCTTCGCGCTGACCCCGAATGCAATTTGCTACAGGCGCAGAACTGGCGCT	3567
QY	3104	GTCGTAAGGGGGCAGAGACCAACAGAAAGGTTCTTGCCGTGATCTCCCATGAGGGGTG	3163
Db	3568	GGCTGGAAGGGGGCAGAGACCAAGAGGGGTTTACCTGTGACTCTTCATCAAGAGGGTGTG	3627
QY	3164	G---CGAGTTCCCTGCTGTCTGTGCCACATGCTGCTGCTGTGTGTGGCAATGGTTAGAAATGGGA	3220
Db	3628	GTTCTGTGTTTTCATCTCTTACAGAGAAAGTCACTCTGTGTGGCGTTGTGAAATGGGA	3687
QY	3221	CACACGCCCCCTGTGTGAGGTTTACATGTGACCTTCTTATAGGTTTAACTGAGTTTGTGG	3280
Db	3688	CACATGCCCC-TGTCTGTAAGTTTACATGTGACCTTCTTGTAGGTTAACTTGATTTCTGTAG	3746
QY	3281	CCTGGGACACATGTATGAAAGTGCACAGTCCACAGGTGACAGAGAAATCCAACTGTGGA	3340
Db	3747	CTTGGGAACCCGTATATGAAGGTTAACGTCCACAGGTGATGAGAAATTCAGGCTGTAG	3806
QY	3341	TTTACAGGTGCATACAGGATGATCTCTTTCAAGTCTATCTGGGGGACATAGGTGAGTCTGC	3400
Db	3807	TTTACAGGTGCACTCAAGTGTGTTCAATTCAGTTTACTGGGGGAGATGAGGTGAGTCAAGC	3866
QY	3401	TTCACCTCAGAAAGGAAGATTCCTTGCCCTTCATCCAGGGGACACAGGGTACATCCCAAGGC	3460
Db	3867	TTCACGAGGAAGGAAGCAATACCTTGCCCTTCATTAAGGGGACACAGGGTACATCCCAAGGC	3926
QY	3461	ATCCGGGGAACGTGAAGCTCTCACTTCAAAACCATGTCAAGAAATTTAAAAACACTCCCTCC	3520
Db	3927	ATCAGAAATCTGCGAG--CTCACTCTCAAAACCATGTCAAGAAATTTAAAAACAACCCCATCC	3984
QY	3521	CCTCACTGTAGCCTTTCGGCAACTGCGCCCAATCCCTTTATATCAAAAGAAATTAAGTAAAG	3580
Db	3985	CCTCACTGTAGCCTTTTGCAAACTTGTGCCAAACCTTCAACAAGAAATTTAAAGTAAAG	4044
QY	3581	CATATAAATTTAAAAAATTTAAAAA 3606	
Db	4045	CGTATTAATTTCTTCACAGCAAGCAA 4070	
RESULT 7			
ADT92216			
ID	ADT92216	standard; cDNA; 2497 BP.	
XX	ADT92216;		
XX	AC		
XX	DT	13-JAN-2005 (first entry)	
XX	DE	Murine phosphodiesterase 10A7 (PDE10A7) encoding cDNA.	
XX	KW	PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;	
XX	KW	neuroprotective; gene therapy; transgenic; gene; ss; mouse.	
XX	MS	Mus musculus.	
XX	Key	Location/Qualifiers	
XX	PH		

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FT CDS 77..2470
FT /tag= a
FT /product= "PDE10A7"
FT /note= "phosphodiesterase 10A7"
XX
XX WO2004090126-A2.
XX
XX 21-OCT-2004.
XX
XX 30-MAR-2004; 2004WO-US009878.
XX
XX 03-APR-2003; 2003US-0459603P.
XX
XX (MEMO-) MEMORY PHARM CORP.
XX
XX Wang D, Bugaj-Gaweda B;
XX
XX MPI; 2004-748763/73.
XX
XX P-PSDB; ADT92217.
XX
XX New isolated polynucleotide comprising a polynucleotide sequence coding
XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
XX creating or preventing memory, psychiatric or cognitive disorders.
XX
XX Claim 2; SEQ ID NO 1; 93pp; English.
XX
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders. The
XX present sequence represents a cDNA encoding a mouse PDE10A7 enzyme.
XX
XX Sequence 2497 BP; 639 A; 659 C; 651 G; 548 T; 0 U; 0 Other;
XX
XX Query Match 65.0%; Score 2344.8; DB 13; Length 2497;
XX Best Local Similarity 98.9%; Pred. No. 0;
XX Matches 2361; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
XX
XX 488 TGCCTCCGAAGGCTGACCGAGTGTCTCTCAGCCCGCAGTTGACGATGAAAGGTGAG 547
XX |||||
XX 110 TGCCTCCGCTTCCCAAGCCCTCTGCTACCAACAAGTTTGAGATGAAAGGTGAG 169
XX |||||
XX 548 GCGTATCTTCTCTCATCCAGGATTTAGATGAAATTTGTTCTGAAAGTTTATGCA 607
XX |||||
XX 170 GCGTATCTTCTCTCATCCAGGATTTAGATGAAATTTGTTCTGAAAGTTTATGCA 229
XX |||||
XX 608 GAGCTGTGAAAAAGTGGCTGAAAGAGAAACCAAGCAAAAGAAAGTAAACCATCTCC 667
XX |||||
XX 230 GAGCTGTGAAAAAGTGGCTGAAAGAGAAACCAAGCAAAAGAAAGTAAACCATCTCC 289
XX |||||
XX 668 AAGGAAGTCAGCAGGTACAGAGATACGAATATGCAAGGAGTCTGTACGAGCTGAACGC 727
XX |||||
XX 290 AAGGAAGTCAGCAGGTACAGAGATACGAATATGCAAGGAGTCTGTACGAGCTGAACGC 349
XX |||||
XX 728 TACATGAGCAGCGCTGAGACGCGCGGGGACCAACCACTGCTCTCTATGAGCTCAGC 787
XX |||||
XX 350 TACATGAGCAGCGCTGAGACGCGCGGGGACCAACCACTGCTCTCTATGAGCTCAGC 409
XX |||||
XX 788 AGCATCATCAGGAATAGCCAAAGCCGAGATTGCACTGTACTTCTTGAGAGTGC 847
XX |||||
XX 410 AGCATCATCAGGAATAGCCAAAGCCGAGATTGCACTGTACTTCTTGAGAGTGC 469
XX |||||
XX 848 AATAATAGCTGTGTGTTGATACCAACCCGAGATGAAAGAGCAACCCCGCTCATC 907
XX |||||
XX 470 AATAATAGCTGTGTGTTGATACCAACCCGAGATGAAAGAGCAACCCCGCTCATC 529
XX |||||
XX 908 CTCGAGGGGCCATCACCAGGGTACCAACATCTGCTCTACGTCGCAATGCTTAGAAG 967
XX |||||

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Db 530 CCTGCAAGGGCCATCACCAGGGTACCAACATCTCTGCTACGTGCGCAAGTCTAGAAAG 589
Qy 968 AGCTGTGTGTAAGAGATATCTTTGGGATGAGCGAATTTCTCGAGGTACTGGCCCTGAA 1027
Db 590 AGCTGTGTGTAAGAGATATCTTTGGGATGAGCGAATTTCTCGAGGTACTGGCCCTGAA 649
Qy 1028 TCAGGAACCCGCATCAGTCTGTTCTTTGCTTGCCCATTTGTCATGCTGCCATTGGAAGCTTG 1087
Db 650 TCAGGAACCCGCATCAGTCTGTTCTTTGCTTGCCCATTTGTCATGCTGCCATTGGAAGCTTG 709
Qy 1088 ATTGGCATCTTGAACCTGTACAGGACCTGGGGCAAGAGGAGGCTTGTGCTCAACCATCAG 1147
Db 710 ATTGGCATCTTGAACCTGTACAGGACCTGGGGCAAGAGGAGGCTTGTGCTCAACCATCAG 769
Qy 1148 GAGTTGCAACGCCAATTTGCTGGGTTTCCGTAGCAATACACAGGTGAGAGGTGT 1207
Db 770 GAGTTGCAACGCCAATTTGCTGGGTTTCCGTAGCAATACACAGGTGAGAGGTGT 829
Qy 1208 AAGAGTCTGCCAAGCAGACCGAATGAACTTCTCTACTGACGATCAAGACATAC 1267
Db 830 AAGAGTCTGCCAAGCAGACCGAATGAACTTCTCTACTGACGATCAAGACATAC 889
Qy 1268 TTTGATTAACATAGTTGCTGATAGCTCTTACTTGAACATCATGATATATGCAAAAAAT 1327
Db 890 TTTGATTAACATAGTTGCTGATAGCTCTTACTTGAACATCATGATATATGCAAAAAAT 949
Qy 1328 CTAGTGAACGCCGACCGCTGCGCTCTTCCAGTGTGACCAAGAACAGAGCTGTAC 1387
Db 950 CTAGTGAACGCCGACCGCTGCGCTCTTCCAGTGTGACCAAGAACAGAGCTGTAT 1009
Qy 1388 TCGGACCTGTTGACATTTGGGGAGAGAGAGGAGGAGCCCATCTTCAAGAGAACCAAG 1447
Db 1010 TCGGACCTGTTGACATTTGGGGAGAGAGAGGAGGAGCCCATCTTCAAGAGAACCAAG 1069
Qy 1448 GAGATCAGATTTTCCATTGAGAAAGGATGCTGTCAAATGTGCAAGAACAGGCAAGTC 1507
Db 1070 GAGATCAGATTTTCCATTGAGAAAGGATGCTGTCAAATGTGCAAGAACAGGCAAGTC 1129
Qy 1508 TTGAACATTCGCCGATGCTTACCGGACCTCGTTTAAACAGGAGGTGACCTGTACAC 1567
Db 1130 TTGAACATTCGCCGATGCTTACCGGACCTCGTTTAAACAGGAGGTGACCTGTACAC 1189
Qy 1568 GGTACACCAACGAGGAACATTTGTTATGCCATAGTAGAGCCGAGGACGCTGATTTGC 1627
Db 1190 GGTACACCAACGAGGAACATTTGTTATGCCATAGTAGAGCCGAGGACGCTGATTTGC 1249
Qy 1628 GTGATGAGATGTGTGAACAAGATCAGCGTAGCGCTTCTTCAAGACAGACGAACAC 1687
Db 1250 GTGATGAGATGTGTGAACAAGATCAGCGTAGCGCTTCTTCAAGACAGACGAACAC 1309
Qy 1688 TTCAAGATTTTGTCTGTCTTGTGCGACCTGGCTTGACCTGTCTTAAATGTACACAG 1747
Db 1310 TTCAAGATTTTGTCTGTCTTGTGCGACCTGGCTTGACCTGTCTTAAATGTACACAG 1369
Qy 1748 ATCCGCACTCAGAAATGCACTTACAGGTTTACATGAGAAAGCTTCTCTACACAGATC 1807
Db 1370 ATCCGCACTCAGAAATGCACTTACAGGTTTACATGAGAAAGCTTCTCTACACAGATC 1429
Qy 1808 TGCACCTCCGAGAGATGAGCAAGGCTCATGCGCTTCAACCTTACAGACGACATCTGCGG 1867
Db 1430 TGCACCTCCGAGAGATGAGCAAGGCTCATGCGCTTCAACCTTACAGACGACATCTGCGG 1489
Qy 1868 GACATGAGATTTTCACTTTGACATTTGCTTTTGAAGAACATGTGGCTGTGGATCTTT 1927
Db 1490 GACATGAGATTTTCACTTTGACATTTGCTTTTGAAGAACATGTGGCTGTGGATCTTT 1549
Qy 1928 GTCTACATGATCCATCGCTCTGTGGGACATCCGTTTGAACCTTGAAGAAATTTGTGCGT 1987
Db 1550 GTCTACATGATCCATCGCTCTGTGGGACATCCGTTTGAACCTTGAAGAAATTTGTGCGT 1609
Qy 1988 TTTATCATGTCTGTGAAGAAAGTATCGCGGATTCCTTACCAACATGGAAGCATGCA 2047
Db 1610 TTTATCATGTCTGTGAAGAAAGTATCGCGGATTCCTTACCAACATGGAAGCATGCA 1669

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OY 2048 GTACAGGTGGCAGACGTATGTCATATCTTCAAAAACAAGATGGCCTTTCAAGAC 2107
DB 1670 GTACAGGTGGCAGACGTATGTCATATCTTCAAAAACAAGATGGCCTTTCAAGAC 1729
OY 2108 CTGAGCGCAAAAGGCTGTAAATTGCTGTCTGTGTCATGACCTGAGCCAGAGGGCTTC 2167
DB 1730 CTGAGCGCAAAAGGCTGTAAATTGCTGTCTGTGTCATGACCTGAGCCAGAGGGCTTC 1789
OY 2168 AGTACAGGTACTGTGCAAGAAAGTTCCACCCCTGTGCGCGCTGTACTTCCACTTCCACC 2227
DB 1790 AGTACAGGTACTGTGCAAGAAAGTTCCACCCCTGTGCGCGCTGTACTTCCACTTCCACC 1849
OY 2228 ATGAGCAACACCACTTCTCCAGACGGGTGTCTCTTCACTGAGTGAAGGAGCAATATC 2287
DB 1850 ATGAGCAACACCACTTCTCCAGACGGGTGTCTCTTCACTGAGTGAAGGAGCAATATC 1909
OY 2288 TTCTCCACCTGTAGCTCCAGACGAGTACGAGCAGGTGCTGAGATCATCCGCAAAAGCCATC 2347
DB 1910 TTCTCCACCTGTAGCTCCAGACGAGTACGAGCAGGTGCTGAGATCATCCGCAAAAGCCATC 1969
OY 2348 ATGCGCACGACCTGTGCTTATCTTTGGGAAACAGAAACAGTTGAGAGATGTAACG 2407
DB 1970 ATGCGCACGACCTGTGCTTATCTTTGGGAAACAGAAACAGTTGAGAGATGTAACG 2029
OY 2468 ACAGGGGTGCGAAGCTCCACCAACAGTCCCATGCGACCGTGTCACTGGCTTGATGATG 2467
DB 2030 ACAGGGGTGCGAAGCTCCACCAACAGTCCCATGCGACCGTGTCACTGGCTTGATGATG 2089
OY 2468 ACTGCTGTGATCTTGTCTGTGTGACCAAACTATGCGCAGTTACAAATTTGACAGCGAT 2527
DB 2090 ACTGCTGTGATCTTGTCTGTGTGACCAAACTATGCGCAGTTACAAATTTGACAGCGAT 2149
OY 2528 GATATATATGCAAGATTTCTGGGCTGAGGGTGTAGATGAAGAAGCTGGGCATACAGCCC 2587
DB 2150 GATATATATGCAAGATTTCTGGGCTGAGGGTGTAGATGAAGAAGCTGGGCATACAGCCC 2209
OY 2588 ATTCTATGATGAGACAGACAAAGCAGATGAAGTCCCTCAAGGGCAGCTCGGATTTCTAC 2647
DB 2210 ATTCTATGATGAGACAGACAAAGCAGATGAAGTCCCTCAAGGGCAGCTCGGATTTCTAC 2269
OY 2648 AATGCTGTGCGCATTCCTCTGTATACCACTTGAACGAGATCTTCCACCAACAGACCT 2707
DB 2270 AATGCTGTGCGCATTCCTCTGTATACCACTTGAACGAGATCTTCCACCAACAGACCT 2329
OY 2768 CTGCTGAAGGCTCTGACGAGATTAACCTCAATCACTGAGAGAAAGTAAATTGCGGGGAAAG 2767
DB 2330 CTGCTGAAGGCTCTGACGAGATTAACCTCAATCACTGAGAGAAAGTAAATTGCGGGGAAAG 2389
OY 2768 ACAGCAATGTGATTTCAAGGCCAGGCCCGGCGCTAGACAGACCAACCTGAGAAGCTG 2827
DB 2390 ACAGCAATGTGATTTCAAGGCCAGGCCCGGCGCTAGACAGACCAACCTGAGAAGCTG 2449
OY 2828 AACGTGAAGTTGAAGACTGATCTGAAGTGAAGTCTGTGATGTCTGCGC 2875
DB 2450 AACGTGAAGTTGAAGACTGATCTGTGAAGTGAAGTCTGTGATGTCTGCGC 2497

RESULT 8
ADT92218
ID ADT92218 standard; cDNA; 2560 BP.
XX
XX ADT92218;
XX
XX 13-JAN-2005 (first entry)
XX
XX Rat phosphodiesterase 10A7 (PDE10A7) encoding cDNA.
XX
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; noctropic;
XX neuropeptide; gene therapy; transgenic; gene; ss; rat.
XX
XX Rattus norvegicus.
XX

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FH Key Location/Qualifiers
FT CDS 71..2458
FT /tag=a
FT /product="PDE10A7"
FT /note=" phosphodiesterase 10A7"

W02004090126-A2.
21-OCT-2004.
30-MAR-2004; 2004MO-US009878.
03-APR-2003; 2003US-0459603P.
(MEMO-) MEMORY PHARM CORP.
Wang D, Bugaj-Gaweda B;
WPI; 2004-748763/73.
P-PSDB; ADT92219.

PT New isolated polynucleotide comprising a polynucleotide sequence coding
PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for
PT treating or preventing memory, psychiatric or cognitive disorders.
XX
XX Claim 3; SEQ ID NO 3; 93pp; English.
XX
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or GMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders. The
XX present sequence represents a cDNA encoding a rat PDE10A7 enzyme.
SQ Sequence 2560 BP; 654 A; 675 C; 664 G; 567 T; 0 U; 0 Other;

Query Match 60.1%; Score 2167; DB 13; Length 2560;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 2270; Conservative 0; Mismatches 115; Indels 14; Gaps 2;

OY 505 GTTTGACGAGTGAAGGATGAAGGCTTATCTTCTCATCCCAAGGATTAAGTGAAT 584
DB 141 GCTTACGATGAAGGATGAAGGCTTATCTTCTCATCCCAAGGATTAAGTGAAGT 200
OY 585 TTGTTTCTGAAGTGTATGTCAGAGACTGTGAAGAGTGGCTGAAGAGAAACCAACA 644
DB 201 TTGTTTCTGAAGTGTATGTCGAGAGACTGTGAAGAGTGGCTGAAGAGAAACCAACA 260
OY 645 AAGCAAAAGATGAACATCTTCCAGAAAGTCAAGAGTACAGATACGAATATGACAG 704
DB 261 AAGCAAAAGATGAACATCTTCCAGAAAGTCAAGAGTACAGAGTACAGAAATGACAG 320
OY 705 GAGTGTGTAGAGGTGAAGAGCTTACATAGAGCAGCGCTGGAACACGGGCGGAGCAAC 764
DB 321 GAGTGTGTAGAGGTGAAGAGCTTACATAGAGCAGCGCTGGAACACGGGCGGAGCAAC 380
OY 765 ACTGCTCTCTATAGCTCAGACGATCATCAGATTAAGCAACAAAGCCGAGATTG 824
DB 381 ACTGCTCTCTATAGCTCAGACGATTAAGCAAGTATCAGATTAAGCAACAAAGCCGAGATTG 440
OY 825 CACTGACTTCTTGTGAGAGTGAATTAATAGCTGTGTGTGTTCAATACCAACCCGAGATGA 884
DB 441 CACTGACTTCTTGTGAGAGTGAATTAATAGCTGTGTGTGTTCAATACCAACCCGAGATGA 500
OY 885 AGGAAGGCAACCCCGGCTATCCCTGAGAGGCGCATACCAAGGATTCACCATCTCG 944
DB 501 AGGAAGGCAACCCCGGCTATCCCTGAGAGGCGCATACCAAGGATTCACCATCTCTG 560
OY 945 CTAAGTGGCAAGTCTAGAAAGCTTTGTTGATGAGATATCTTGGGAGTGAAGCAT 1004

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DB ||||| 561 CCTATGTCGCCAGTCTAGAGAACCTGCTGTGTAGAGACATCTTGGGAGTGGCAT 620  
QY ||||| 1005 TTCCCTGAGGTATCTGGCCCTGGAAATCAGGAACCGGATCCAGTCTGTCTTGGCCCA 1064  
DB ||||| 621 TTCCAGAGGCACTGAGTCTGAGGTCAAGGAACCGAATCCAGTCTGTCTTGGCCCA 680  
QY ||||| 1065 TTGTCACTGCCATTTGGAAGCTTGAATTTGGCATCTTGAACCTGTACAGGCACTG 1124  
DB ||||| 661 TTGTCACTGCCATTTGGAAGCTTGAATTTGGCATCTTGAACCTGTACAGGCACTG 740  
QY ||||| 1125 AGGCTTCTGCTCAGCCATCAGAGGTTGCAACCGCAATCTGCTTGGGCTTCCGTA 1184  
DB ||||| 741 AGGCTTCTGCTCAGCCATCAGAGGTTGCAACCGCAATCTGCTTGGGCTTCCGTA 800  
QY ||||| 1185 CAATACACAGGTGAGGTGTAGAGTCTGCGCAACAGACCGAATGAACTTCC 1244  
DB ||||| 801 CAATACACAGGTGAGGTGTAGAGTCTGCGCAACAGACCGAATGAACTTCC 860  
QY ||||| 1245 TACTGACGTATCAAGACATCTTGTATACATAGTTGCCATAGACTCTTATGAA 1304  
DB ||||| 861 TGTCTGATGTATCAAGACATCTTGTATACATAGTTGCCATAGACTCTTATGAA 920  
QY ||||| 1305 ACATCATGATATATGCAAAAAATCTAGTAAACGCGCAGCGCTGCTTCCAGTGG 1364  
DB ||||| 921 ACATCATGATATATGCAAAAAATCTAGTAAACGCGCAGCGCTGCTTCCAGTGG 980  
QY ||||| 1365 ACCACAGAAACAAGGCTGTACTGCGACTGTTGCAATGGGGAGGAAGAGGGGA 1424  
DB ||||| 981 ACCACAGAAACAAGGCTGTACTGCGACTGTTGCAATGGGGAGGAAGAGGGGA 1040  
QY ||||| 1425 AGCCCATCTTCAAGAGACCAAGAGATCAGATTTTCCATTGGAAGAGGATGCTGTC 1484  
DB ||||| 1041 AGCCCATCTTCAAGAGACCAAGAGATCAGATTTTCCATTGGAAGAGGATGCTGTC 1100  
QY ||||| 1485 AAGTGCAGAGAAACAGGCGAAGTCTTGAACATTTCCGATGCTTACGCGCACTCTGCTTAA 1544  
DB ||||| 1101 AAGTGCAGAGAAACAGGCGAAGTCTTGAACATTTCCGATGCTTACGCGCACTCTGCTTAA 1160  
QY ||||| 1545 ACAGGAGGTGGAACCTGTACACAGGCTTACACAGGAGAACATTTGATATGCGCATG 1604  
DB ||||| 1161 ACAGGAGGTGGAACCTGTACACAGGCTTACACAGGAGAACATTTGATATGCGCATG 1220  
QY ||||| 1605 TGAAGCGGAGAGCTGATTTGCGGTGTGAGATGAGTGAACAAGATCAGCGTACGCTTGC 1664  
DB ||||| 1221 TGAAGCGGAGAGCTGATTTGCGGTGTGAGATGAGTGAACAAGATCAGCGTACGCTTGC 1280  
QY ||||| 1665 TCTTCAAGACAGACGAGAACATTTCAAGATGTTTGTCTTCTGCGCATGCGCTTGC 1724  
DB ||||| 1281 TCTTCAAGACAGACGAGAACATTTCAAGATGTTTGTCTTCTGCGCATGCGCTTGC 1340  
QY ||||| 1725 ACTGTGCTAACATGTACACAGAGTCCGCACTCAGAAATGATCTTACAGGCTTACATG 1784  
DB ||||| 1341 ACTGTGCTAACATGTACACAGAGTCCGCACTCAGAGTGCATCTTACAGGCTTACATG 1400  
QY ||||| 1785 AGAAGCTTCTCAACAGAGTGCATCTCAGAGAGTGCAGAGGCTTACAGGCTTCA 1844  
DB ||||| 1401 AGAAGCTTCTCAACAGAGTGCATCTCAGAGAGTGCAGAGGCTTACAGGCTTCA 1460  
QY ||||| 1845 ACCTACAGCAGCAGATCTGCGGAGACATCGAGCTATTTCACTTGAATGCTTCTTGC 1904  
DB ||||| 1461 ACTTGCAGCAGCAGATCTGCGGAGACATCGAGCTATTTCACTTGAATGCTTCTTGC 1520  
QY ||||| 1905 AGAATCATGTGCTGAGATCTTGTCTTACATGATCCATCGGTCTTGTGGAGCATCTGTT 1964  
DB ||||| 1521 AGAATCATGTGCTGAGATCTTGTCTTACATGATCCATCGGTCTTGTGGAGCATCTGTT 1580  
QY ||||| 1965 TTGAATTTGAAAAATTTGCGGTTTATCATGTCTGTGAAGAACTATCGGCGGTTTC 2024  
DB ||||| 1581 TTGAATTTGAAAAATTTGCGGTTTATCATGTCTGTGAAGAACTATCGGCGGTTTC 1640  
QY ||||| 2025 CTTACCAACATGAGACATGCACTGAGTGCAGCTGATGATCCATTTCAAA 2084

DB ||||| 1641 CTTTACCAACTGGAAGCATGCACTGCTGCGCACTGATGTACGCATATCTTCAAA 1700  
QY ||||| 2085 ACAATATGCTCTTTCACAGACTCTGAGCGCAAAAGGCTTCTTAAATGCGTCTGTGCC 2144  
DB ||||| 1701 ACAATATGCTCTTTCACAGACTCTGAGCGCAAAAGGCTTCTTAAATGCGTCTGTGCC 1760  
QY ||||| 2145 ATGACCTGGAACAAGGGGCTTCACTGATACAGCTTACCTGCAAGATTTGCAACCCCTG 2204  
DB ||||| 1761 ATGACCTGGAACAAGGGGCTTCACTGATACAGCTTACCTGCAAGATTTGCAACCCCTG 1820  
QY ||||| 2205 CGGCTGTACTCTCACTTCAACATGAGCAACCACTTCTCCAGACGCTGTCTATCC 2264  
DB ||||| 1821 CTGCTTGTATCTTCACTTCAACATGAGCAACCACTTCTCCAGACGCTGTCTATCC 1880  
QY ||||| 2265 TTGACTGGAAGGCAATATCTTCTCACTTCAAGCTTCAAGCTTCAAGGAGTGC 2324  
DB ||||| 1881 TCCAGCTGGAAGGCAATATCTTCTCACTTCAAGCTTCAAGGAGTGC 1940  
QY ||||| 2325 TGGAGATATCCGCAAGCATATGCGCACCGAATCTGCTTATCTTGGGAAACAGGA 2384  
DB ||||| 1941 TGGAGATATCCGCAAGCATATGCGCACCGAATCTGCTTATCTTGGGAAACAGGA 2000  
QY ||||| 2385 AGCAGTTGGAAGAGATGTACAGAGAGGCTGCTGAACTTCCACAAACAGTCCATCGAG 2444  
DB ||||| 2001 AGCAGTTGGAAGAGATGTACAGAGAGGCTGCTGAACTTCCACAAACAGTCCATCGAG 2060  
QY ||||| 2445 ACCGTGTATCGGCTTGTATGATGACTGCTGTGATCTTGTCTGTGACAAATATGTC 2504  
DB ||||| 2061 ACCGTGTATCGGCTTGTATGATGACTGCTGTGATCTTGTCTGTGACAAATATGTC 2120  
QY ||||| 2505 CAGTTACAAATTTGACAGGAAATGATATATATGAGAAATTCGGGCTGAGGGTGTAGGA 2564  
DB ||||| 2121 CAGTTACAAATTTGACAGGAAATGATATATATGAGAAATTCGGGCTGAGGGGATGAGA 2180  
QY ||||| 2565 TGAAGAGCTGGGCTTACAGCCATTTCTATGATGAGACAGAGCAAGCAGATGAAGTCC 2624  
DB ||||| 2181 TGAAGAGCTGGGCTTACAGCCATTTCTATGATGAGACAGAGCAAGCAGATGAAGTCC 2240  
QY ||||| 2625 CTCAAGGAGCTGAGATTTCAATGCTGTGGCAATTTCTGCTTACACCTTGAACGC 2684  
DB ||||| 2241 CTCAAGGAGCTGAGATTTCAATGCTGTGGCAATTTCTGCTTACACCTTGAACGC 2300  
QY ||||| 2685 AGATCTTCCACCCACAGGCTCTGCTGAAAGGCTGAGGATTAACCTCAATCAGTGG 2744  
DB ||||| 2301 AGATCTTCCACCCACAGGCTCTGCTGAAAGGCTGAGGATTAACCTCAATCAGTGG 2360  
QY ||||| 2745 AGAAGTAAATTTGCGGGAAGAGACAGCAATGTGAATTTCAAGGCCAGGCCCTTA 2804  
DB ||||| 2361 AGAAGTAAATTTGCGGGAAGAGACAGCAATGTGAATTTCAAGGCCAGGCCCTTA 2414  
QY ||||| 2805 GCAAGACACACTTGAAGAGCTGAACGTGAAGTTGAAGATGTATCTGAAGTACGCTCC 2864  
DB ||||| 2415 GCAAGACACACTTGAAGAGCTGAACGTGAAGTTGAAGATGTATCTGAAGTACGCTCC 2466  
QY ||||| 2865 TGAATGTGCTGAGCAACGATCTGATCTTCTGATCTTCTTGTGTTTCA 2923  
DB ||||| 2467 TGAATGTGCTGAGCAACGATCTGATCTTCTGATCTTCTTGTGTTTCA 2525

RESULT 9  
AAA09592  
ID AAA09592 standard; cDNA to mRNA, 3080 BP.  
XX  
AC AAA09592:  
XX  
DT 29-JUN-2001 (first entry)  
XX  
XX Human phosphodiesterase 10 (PDE10) nucleotide sequence S80 ID 4.  
XX  
XX Phosphodiesterase 10; PDE10; human; ss.  
OS Homo sapiens.  
XX



FN JP20024992-A.  
XX 15-AUG-2000.  
XX 11-MAY-1999; 99JP-00129343.  
XX 30-NOV-1998; 98JP-0038861.  
XX (TANA ) TANABE SEIYAKU CO.  
XX WPI; 2000-6b5129/58.  
DR Novel phosphodiesterase and its gene for research on complex mechanism of  
XX intracellular information transfer.  
XX Claim 2; Page 24-27; 29pp; Japanese.  
XX  
XX Sequences ABA09589-A09592 encode human phosphodiesterase 10 (PDE10)  
CC proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful  
CC for research on the complex mechanism of intracellular information  
CC transfer. The invention includes a recombinant vector containing a PDE10  
CC gene, and a cell transformed with the vector. Sequences ABA09593-A09606  
CC represent PCR primers used in the isolation of the PDE10 polynucleotide  
CC sequences of the invention  
XX  
SQ Sequence 3080 BP; 776 A; 826 C; 805 G; 673 T; 0 U; 0 Other;

Query Match 60.1%; Score 2167; DB 3; Length 3080;  
Best Local Similarity 94.6%; Pred. No. 0;  
Matches 2270; Conservative 0; Mismatches 115; Indels 14; Gaps 2;

QY 525 GTTTCACGAGTGAAGAAGGAGGCTATCTTCTCCATCCCGAGTATTAGATGAT 584  
DB 683 GTTTACGGATGAAGAAGGAGGCTATCTTCTCCATCCCGAGTATTAGATGAT 742  
QY 585 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGCTGAGAGAAAACCA 644  
DB 743 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGCTGAGAGAAAACCA 802  
QY 645 AAGCAAAAGATGAACCATCTTCCAGAGAGTCAAGAGTCAAGATGAGATATGCA 704  
DB 803 AAGCAAAAGATGAACCATCTTCCAGAGAGTCAAGAGTCAAGATGAGATATGCA 862  
QY 705 GAGTGTATGAGAGTGAACAGCTACATGAGACGCGCTGAGACGCGCGGGGCAAC 764  
DB 863 GAGTGTATGAGAGTGAACAGCTACATGAGACGCGCTGAGACGCGCGGGGCAAC 922  
QY 765 AACTGCTCTCTATGAGCTCAAGCAGCATCATCAGATAGCCAAAGCCGAGATT 824  
DB 923 AACTGCTCTCTATGAGCTCAAGCAGCATCATCAGATAGCCAAAGCCGAGATT 982  
QY 825 CACTGTACTTCTCTGAGAGTGAATTAATAGCTGTGTGTCTTCAATACCAACCG 884  
DB 983 CACTGTACTTCTCTGAGAGTGAATTAATAGCTGTGTGTCTTCAATACCAACCG 1042  
QY 885 AGGAAGGCAACCCGCGCTATCCCTGACAGGCGCATCACCGAGGTACCAATCT 944  
DB 1043 AGGAAGGCAACCCGCGCTATCCCTGACAGGCGCATCACCGAGGTACCAATCT 1102  
QY 945 CCTAGGTGCGCAAGTCTAGAGAGAGCTGTGTTGTTAGAGATATCTTGGGAGT 1004  
DB 1103 CCTAGGTGCGCAAGTCTAGAGAGAGCTGTGTTGTTAGAGATATCTTGGGAGT 1162  
QY 1005 TTCTCTGAGAGTACTGCGCTGGAATGAGAACCCGCAATCCAGTCTTCTTGG 1064  
DB 1163 TTCTCTGAGAGTACTGCGCTGGAATGAGAACCCGCAATCCAGTCTTCTTGG 1222  
QY 1065 TTGTACATGCGCATTTGGAGATTTGGCATTCCTTGAATGATCAAGGACATGG 1124  
DB 1223 TTGTACATGCGCATTTGGAGATTTGGCATTCCTTGAATGATCAAGGACATGG 1282  
QY 1125 AGGCTTCTGCGCTGAGCATGAGAGTTGCAACGCAATCTTCTTGGGCTTCCGTAG 1184

DB 1283 AGGCTTCTGCGCTGAGCATGAGAGTTGCAACCGCAATCTTCTTGGGCTTCCGTAG 1342  
QY 1185 CAATACACAGGTGAGGTGTGTAGAGTCTTCGCCAAACAGACGGAATGATGATCTCC 1244  
DB 1343 CAATACACAGGTGAGGTGTGTAGAGTCTTCGCCAAACAGACGGAATGATGATCTCC 1402  
QY 1245 TACTGAGCTATCAAGAATATCTTGTATTAATAGTGTGCATAGACTCTCTACTTGAAC 1304  
DB 1403 TGTCTGATGTATCAAGACATCTTGTATTAATAGTGTGCATAGACTCTCTACTTGAAC 1462  
QY 1305 ACATCATGATATATGCAAAAAAATCTAGTGAACCGCGACCGCTGCGCTTCCAGTGG 1364  
DB 1463 ACATCATGATATATGCAAAAAAATCTAGTGAACCGCGACCGCTGCGCTTCCAGTGG 1522  
QY 1365 ACCAACAAGAGAGTGTATCTCGACCTGTGTGATGATTTGGGAGAGAGAGGGGA 1424  
DB 1523 ACCAACAAGAGAGTGTATCTCGACCTGTGTGATGATTTGGGAGAGAGAGGGGA 1582  
QY 1425 AGCCATCTTCAAGAGACCAAGAGATCAATTTTCCATTGAGAAAGGATTTGCTGTC 1484  
DB 1583 AGCCGCTTCAAGAGACCAAGAGATCAATTTTCCATTGAGAAAGGATTTGCTGTC 1642  
QY 1485 AAGTGGCAAGAACAGGCGAATCTTTGAACATTTCCGATGCTTACGCGGACCTGCTT 1544  
DB 1643 AAGTGGCAAGAACAGGCGAATCTTTGAACATTTCCGATGCTTACGCGGACCTGCTT 1702  
QY 1545 AAGAGAGAGTGAACCTGTACACAGGCTACACAGAGAACATCTGTATGCGCATAG 1604  
DB 1703 AAGAGAGAGTGAACCTGTACACAGGCTACACAGAGAACATCTGTATGCGCATAG 1762  
QY 1605 TGAGCCGAGGAGCGTGTATGCGGTGTGTCAGATGCTGTAACAGATCAGCGGTAGCGCT 1664  
DB 1763 TGAGCCGAGGAGCGTGTATGCGGTGTGTCAGATGCTGTAACAGATCAGCGGCT 1822  
QY 1665 TCTCCAGACAGAGAGAACATTTCAAGATTTCTGTCTTCTGCGCACTGCGCTTGC 1724  
DB 1823 TCTCCAGACAGAGAGAACATTTCAAGATTTCTGTCTTCTGCGCACTGCGGCTTGC 1882  
QY 1725 ACTGTGCTAATATGATACAGAGATCCGCGCATGAGATGATCTACAGGGTTACAGTGG 1784  
DB 1883 ACTGTGCTAATATGATACAGAGATCCGCGCATGAGATGATCTACAGGGTTACAGTGG 1942  
QY 1785 AGAAGCTTCTCTACACAGATCTGCACTCGAGAGTGGCAAGCCTCATGCGCTTCA 1844  
DB 1943 AGAAGCTTCTCTACACAGATCTGCACTCGAGAGTGGCAAGCCTCATGCACTTCA 2002  
QY 1845 ACTTACAGACAGCATCTGCGGAGCATGAGCTATTCATCTTGAACATTTGCTCTTTCG 1904  
DB 2003 ACTTACAGACAGCATCTGCGGAGCATGAGCTATTCATCTTGAACATTTGCTCTTTCG 2062  
QY 1905 AGAATATGAGGCTGCGGATCTTTGTCTTACATGATCCATCGGTCTTGGGACATCTGTT 1964  
DB 2063 AGAATATGAGGCTGCGGATCTTTGTCTTACATGATCCATCGGTCTTGGGACATCTGTT 2122  
QY 1965 TTGAATCTGAAGAAATTTGCGGTTTATCATGTCTGTGAAGAAACATTAAGCGGGTT 2024  
DB 2123 TTGAATCTGAAGAAATTTGCGGTTTATCATGTCTGTGAAGAAACATTAAGCGGGTT 2182  
QY 2025 CTTCACACATGAGAGATGAGTCAAGGTGAGACATGAGATGATGATCTTCAAA 2084  
DB 2183 CTTCACACATGAGAGATGAGTCAAGGTGAGACATGAGATGATGATCTTCAAA 2242  
QY 2085 ACAACATGAGGCTTCTTACAGACCTCGAGCGGCAAGGCTGTAAATGCGGTCTGTCG 2144  
DB 2243 ACAACATGAGGCTTCTTACAGACCTGTAGCGCAAGGCTGTAAATGCGGTCTGTCG 2302  
QY 2145 ATGACCTGAGACACAGGGGCTTTCAGTAAACAGCTACTGAGAAATTTGCAACCCCTG 2204  
DB 2303 ATGACCTGAGACACAGGGGCTTTCAGTAAACAGCTACTGAGAAATTTGCAACCCCTG 2362  
QY 2205 CGGCGCTGTACTTCCACCTTCCACATGAGAACCACTTCTCCAGACGCTGTCCATCC 2264  
DB 2363 CTGCGTTGTATCTTCCACCTTCCACATGAGAACCACTTCTCCAGACGCTGTCCATCC 2422



QY 2265 TTCAGCTGGAGAGGCAATATCTTCTCAACCTTGAGCTTCAGAGGATGAGAGAGTGC 2324  
DB 2423 TCCAGCTGGAGAGGCAATATCTTCTCAACCTTGAGCTTCAGAGGATGAGAGAGTGC 2482  
QY 2325 TGGAGATCATCCGCAAGGATCATCTGCGACCGAAGCTTCCCTCTATCTTTGGGAAAGAGA 2384  
DB 2483 TGGAGATCATCCGCAAGGATCATCTGCGACCGAAGCTTCCCTCTATCTTTGGGAAAGAGA 2542  
QY 2385 AGCAGTTGAGAGGATGATCAAGAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAG 2444  
DB 2543 AGCAGTTGAGAGGATGATCAAGAGAGGATGAGAGGATGAGAGGATGAGAGGATGAGAG 2602  
QY 2445 ACCGCTGATCCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2504  
DB 2603 ACCGCTGATCCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2662  
QY 2505 CAGTTACAAATTTGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2564  
DB 2663 CAGTTACAAATTTGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2722  
QY 2565 TGAAGAGCTGGGCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2624  
DB 2723 TGAAGAGCTGGGCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2782  
QY 2625 CTCAAGGAGCTGCGATTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2684  
DB 2783 CTCAAGGAGCTGCGATTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2842  
QY 2685 AGATCTCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2744  
DB 2843 AGATCTCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2802  
QY 2745 AGAAGGATTTCCGCGGAG 2804  
DB 2903 AGAAGGATTTCCGCGGAG 2956  
QY 2805 GCAAGAGCACTGAG 2864  
DB 2957 GCAAGAGCACTGAG 3008  
QY 2865 TGATGCTGCGAG 2923  
DB 3009 TGATGCTGCGAG 3067  
RESULT 10  
ADM34017  
ID ADM34017 standard; cDNA; 4388 BP.  
XX  
AC ADM34017;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE DNA encoding human phosphodiesterase 8A1 (PDE8A1) splice variant.  
XX  
KW seq; EST; expressed sequence tag; gene; phosphodiesterase 8A; PDE8;  
XX  
OS cyclic nucleotide pathway; human.  
XX  
OS Homo sapiens.  
XX  
FH Key 3. .2414 Location/Qualifiers  
XX  
FT CDS /tag=a  
XX  
FT /product= "Splice variant phosphodiesterase 8A1 (PDE8A1)"  
XX  
FT /partial  
XX  
FT /note= "No start codon"  
XX  
XX US2003215919-A1.  
XX  
XX 20-NOV-2003.  
XX  
XX 19-MAY-2003; 2003US-00440998.  
XX  
XX

XX 16-OCT-1997; 97US-00951648.  
PR 16-OCT-1998; 98US-00174437.  
PR 11-OCT-2000; 2000US-00686055.  
XX  
XX (Lough/ ) LOUGHNEY K.  
XX  
XX Loughney K;  
XX  
XX WPI; 2004-021844/02.  
DR P-PSDB; ADM34018.  
XX  
PT New phosphodiesterase 8 (PDE8) polypeptide, useful in preparing a  
PT composition for treating conditions associated with aberrant cyclic  
PT nucleotide pathways.  
XX  
XX Claim 7; SEQ ID NO 3; 39pp; English.  
XX  
XX The invention relates to purified and isolated phosphodiesterase 8 (PDE8)  
XX polypeptides and polynucleotides. Also described is a method of  
XX identifying a specific binding partner compound of a PDE8 polypeptide or  
XX polynucleotide comprising: (i) contacting the polypeptide or  
XX polynucleotide with a compound; (ii) detecting binding of the compound to  
XX the polypeptide or polynucleotide; and (iii) identifying the compound as  
XX a specific binding partner. The specific binding partner enhances or  
XX inhibits expression of the PDE8 polypeptide or polynucleotide. The  
XX phosphodiesterase 8 (PDE8) polypeptide is useful in preparing a  
XX composition for treating conditions associated with aberrant cyclic  
XX nucleotide pathways. The present sequence represents the coding sequence  
XX of human PDE8A1, a splice variant of PDE8.  
SQ Sequence 4388 BP; 1315 A; 922 C; 920 G; 1231 T; 0 U; 0 Other;  
Query Match 51.9%; Score 1871.8; DB 12; Length 4388;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;  
QY 415 CTTCCCTCTGCGACCGCTTGGCGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTT 474  
DB 2 CTTCCGCTCTGCGCGCGCGCGCGCGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTT 61  
QY 475 TAAACAATGCAAGTGTGCTTCCGAGAGCTGACCGAGTGTTCCTGAGCCCGAGTTTGACGA 534  
DB 62 TAAATAATGCAAGTGTGCTTCCGAGAGCTGACCGAGTGTTCCTGAGCCCGAGTTTGACGA 121  
QY 535 TGAAGAGTGAAGGCTTATCTTCTCTCATCCCGAGATTTAGATGAATTTGTTTGA 594  
DB 122 TGAAGAGTGAAGGCTTATCTTCTCTCATCCCGAGATTTAGATGAATTTGTTTGA 181  
QY 595 AAGTGTATGTCAGAGAGCTGTGAAAAAGTGTGAAAAAGTGTGAAAAAGTGTGAAAAAGTGTG 654  
DB 182 AAGTGTATGTCAGAGAGCACTAGAGAAATGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 241  
QY 655 TGAACCATCTCCAGAGAGTCAAGAGAGTCAAGAGATACAGATATGAGAGAGTGTGTA 714  
DB 242 TGAATCGGCTCTTAAGAGAGTCAAGAGAGTCAAGAGATACAGATATGAGAGAGTGTGTA 301  
QY 715 CGAGCTGAACAGCTATCATAGAGAGCGCTGACACAGCGGCGGAGAGAGAGAGAGAGAGAGAG 774  
DB 302 TGAACCTAAACAGCTATATTAAG 361  
QY 775 CTATGAGCTGAGAGAGCTATCATAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834  
DB 362 CTATGAGCTGAGAGAGCTATTAAG 421  
QY 835 CTTGAG 894  
DB 422 CTTGAG 481  
QY 895 ACCCGGCTCATCCCTGAG 954  
DB 482 ACCCGGCTCATCCCTGAG 541

QY 955 CAAGCTAGAGAGAGCTTTGGTAGAGATATCTTGGGAGTAGACGATTTCTCGAGG 1014  
 DB 542 CAAGTTCAGAGAAAACACTCTAGTAGAGACATCTTGGAGATGAAAGATTTTCCAAAGG 601  
 QY 1015 TACTGGCTGGAATCAGAAACCCGATCCAGTCTGTTCTTTGCTTCCATTTGCACTGC 1074  
 DB 602 TACTGAGACTGGAATCAGGGACTGTAATCAGTCTGTTCTTTGCTTAAACAATGTGCACTGC 661  
 QY 1075 CATTGGAGACTTGGATTTGGATCTTGAAGTATCAGGCACTGGGGCAAGAGCCCTTCG 1134  
 DB 662 AATTGTGTACTGATTTGATTTCTGAGCTGATCGGCACTG3GGCAAGAGAAAGCCCTTCG 721  
 QY 1135 CCTCAGCCATCAGAGAGTTGCAACAGCCATCTTGG3CTTCGTAATACCA 1194  
 DB 722 TCTTAGTACCAAGAGTTGGCAACAGAAATCTTGCTGGGCTTCAATAGCAATACATA 781  
 QY 1195 GGTGCAAGTGTGTAGAGGTCTGCGCAACAGACCGAATGAAATGACTTCTTACTGACGT 1254  
 DB 782 GGTGCAAGTGTGTAGAGGTCTGCGCAACAGACCGAATGAAATGACTTCTTACTGACGT 841  
 QY 1255 ATCAAAAGACTCTTGGATTAACATAGTTGCCATAGCTCTCTACTTGAACATCATGAT 1314  
 DB 842 ATCAAAACATATTTTGTATTAACATAGTTGCCAATAGATTTCTTACTTGAACATCATGAT 901  
 QY 1315 ATATGCAAAAATCTAGTGAAGCCGACCGCTGCGGCTCTTCCAGTGTGACCAACAAG 1374  
 DB 902 ATATGCAAAAATCTAGTGAAGCCGACCGCTGCGGCTCTTCCAGTGTGACCAACAAG 961  
 QY 1375 CAAGAGCTGTACTCGGACTTGTGTCATTTGGGAGAGAGAGAGGAGAGCCCATCTT 1434  
 DB 962 CAAGAGTGTATTTTCAAGACCTTTTGTATTTGAGAGAGAAAGAGAAACCTGTCTT 1021  
 QY 1435 CAAGAGAGCAAGAGAGATCATGTTTTCCATTGAGAAAGGATTTGCTGTGCAATGTGCAAG 1494  
 DB 1022 CAAGAGAGCAAGAGAGATCATGTTTTCAATTTGAGAAAGGATTTGCTGTGCAATGTGCAAG 1081  
 QY 1495 AACAGGCAAGCTTGAACATTTCCGAGTCTACGCGGACCTTCCCTTTAAAGAGGAGGT 1554  
 DB 1082 AACAGGCAAGCTTGAACATTTCCGAGTCTACGCGGACCTTCCCTTTAAAGAGGAGGT 1141  
 QY 1555 GAGACTGTACAGAGGCTACACCAAGAGAAATTTGTGTATGCTTATAGTGAAGCCGAGG 1614  
 DB 1142 GAGACTGTACAGAGGCTACACCAAGAGAAATTTGTGTATGCTTATAGTGAAGCCGAGG 1201  
 QY 1615 CAGCGTGTATGGCGTGTGTCAGATGTGAAACAAGATCAGCGGTAGGCGCTTTTCCAAAGC 1674  
 DB 1202 CAGCGTGTATGGCGTGTGTCAGATGTGAAACAAGATCAGCGGTAGGCGCTTTTCCAAAGC 1261  
 QY 1675 AGACGAGAACAACTTCAAGATGTTTGTCTGTCTTGTGCGCACTGCGCTTGACTGTGCTAA 1734  
 DB 1262 AGATGAAAACAACTTCAAAATGTTTGTCCCTTTTGTGTGCTTAACTTGACTGTGCTAA 1321  
 QY 1735 CATGTACCAAGAGATCCGCACTCAGAAATGATCTACAGGGTTACCATGAGAGCTTTTC 1794  
 DB 1322 TATGTATATTAATAATTCGCCCATCTCAGAGTGCATTTTACCGGGTATACGATGAAAAGCTGTC 1381  
 QY 1795 CTACCAAGACATCTGCACTCTCGAAGAGTGTGCAAGGCTCATGCGCTTCAACTTACAGC 1854  
 DB 1382 CTACCAATAGCAATTTTACTTCAAGAAAGTGTGCAAGGCTCATGCAATTCACCTTCCCGT 1441  
 QY 1855 AGCATGTGCGCGGAGCATGAGCTATTCACCTTTGACATTTGCTTTGAGAAACATGTC 1914  
 DB 1442 GCGTCTTCCGCAAGAAATTTGAATTTATTCACCTTTGACATTTGCTTTTGAAGAACTGTG 1501  
 QY 1915 GCGTGGGATCTTTGTCTACATGATCATCGGTCTTGTGGGACATCTGTTTTGAACCTTGA 1974  
 DB 1502 GCGTGGAAATTTTGTCTACATGATCATCGGTCTGTGTGGACATCTGTCTTTGAGCTTGA 1561  
 QY 1975 AAAAATTTGCGCTTTTATCATGTCTGTGAAGAAACTATGTGGCGGGTCTTTACCAAA 2034  
 DB 1562 AAAAGTTGTCTTTTATATGTCTGTGAAGAAACTATGTGGCGGGTCTTTATACAA 1621  
 QY 2035 CTGGAAGCATGAGTCAAGGTGTGCACTGCAATGTATGCAATCTTCAAAAACAACATG 2094

DB 1622 CTGGAAGATGCGGTGCACTGTAGACACATCGATGTATCCATCTTCAAGAAACAATCACAC 1681  
 QY 2095 CCTCTTCAACAACCTTCGAGCCCAAGAGCCCTGTAAATTCGCTGTCTGTCCCATGACTGGA 2154  
 DB 1682 GCTTTTCAACAACCTTGTAGCCGAAAGGACTGTGTATCTGTCTGTCTGTCTGTCTGTGA 1741  
 QY 2155 CCAAGAGGGCTTCAAGTAACTGACCTGACAGAGTTTCCAGACACCCCTGTGGCGGCTGTGA 2214  
 DB 1742 CCAAGAGGGCTTCAAGTAACTGACCTGACAGAGTTTCCAGACACCCCTGTGGCGGCTGTGA 1801  
 QY 2215 CTCCACTTCCACCATGAGACCAACCACTTCTTCCAGAGGCTTCATCTTCACTGGA 2274  
 DB 1802 CTCCACTTCCACCATGAGACCAACCACTTCTTCCAGAGGCTTCATCTTCACTGGA 1861  
 QY 2275 AGGGCAAAATCTTCTTCCACCTGAGGCTTCCAGAGGATACAGAGAGGCTGTGAGATCAT 2334  
 DB 1862 AGGGCAAAATCTTCTTCCACCTGAGGCTTCCAGAGGATACAGAGAGGCTGTGAGATCAT 1921  
 QY 2335 CCGCAAGCCCATCATCTGCGACCGACCTGCGCTTATCTTTGG3AAACAGAAAGAGTTGGA 2394  
 DB 1922 CCGCAAGCCCATCATCTGCGACCGACCTGCGCTTATCTTTG3AAACAGAAAGAGTTGGA 1981  
 QY 2395 GAGATGTACCAAGACAGGGTGTGTAACCTTCCACCAACCAAGTCCCATGAGACCGTGTAT 2454  
 DB 1982 AGATGTATACCAAGACCGGATCATTAACCTTAAATATCAATCACTAAGACCGGTATAT 2041  
 QY 2455 GCGCTGTATGTATGACTGCTGTGTATCTTTGCTCTGTGACAAACATATGCGCATTTACAA 2514  
 DB 2042 TGTGTGTATGTATGACTGCTGTGTATCTTTGCTGTGTGCAAAACCTGTGCGCTTACAA 2101  
 QY 2515 ATTTGACAGGATGTATATATATGAGAAATTTCTGGCTGAGGGTGTATGATGAAGAGCT 2574  
 DB 2102 ATTTGACAGGATGTATATATATGAGAAATTTCTGGCTGAGGGTGTATGATGAAGAGCT 2161  
 QY 2575 GGGCATACAGCCCATCTTATGTATGATGACAGAGACAAAGCGAGATGAAGTTCCTCAAGGCA 2634  
 DB 2162 GGGATTAACAGCTTATCTTATGATGACAGAGACAAAGAGATGAAGTTCCTCAAGGCA 2221  
 QY 2635 GCTCGGATTTCTTCAATGTGTGTGCGCAATTCCTGCTATACACTTGAAGCGAGATCTTCC 2694  
 DB 2222 GCTTGGGTTTCAATGTGTGTGCGCAATTCCTGCTATACACTTGAAGCGAGATCTTCC 2281  
 QY 2695 ACCGACAGAGCCTTGTGTAAGGCTGTGAGGAGATTAACCTCATCATGTGGAGAGATAT 2754  
 DB 2282 TCCACAGAGCCTTCTTGAAGGATGTGAGGAGATATCTCACTCATGTGGAGAGATAT 2341  
 QY 2755 TCGCGGGAGAGACAGCAATGTGATTTCAAGCCCAAGGCCCGGCGC 2801  
 DB 2342 TCGAGGGAGAGAGACTGCAACTGTGATTTCAATCCCATCGGTGCTC 2388

RESULT 11  
 AAX36711  
 ID AAX36711 standard; DNA; 4389 BP.  
 XX  
 AC AAX36711;  
 XX  
 DT 14-JUL-1999 (first entry)  
 XX  
 DE Human phosphodiesterase, pDE8, coding sequence.  
 XX  
 KW Phosphodiesterase 8; pDE8; human; cyclic nucleotide pathway; therapy;  
 KM intracellular cyclic nucleotide level modulation; cAMP; cGMP; ss.  
 OS Homo sapiens.  
 PN W09919495-A1.  
 XX  
 PD 22-APR-1999.  
 XX  
 PF 16-OCT-1998; 98WO-US021956.  
 XX

PR 16-OCT-1997; 97US-00951648.  
 XX (ICOS-) ICOS CORP.  
 XX  
 PI Longhney K;  
 XX WPI; 1999-277645/23.  
 XX P-PSDB; AAY13935.  
 DR  
 XX  
 PT New isolated phosphodiesterase genes and polypeptides for identifying  
 specific binding partners.  
 PS  
 XX  
 PS Claim 7, Page 50-55; 80pp; English.

This sequence encodes the human phosphodiesterase 8 (PDE8) of the invention. The phosphodiesterase genes and polypeptides are used to develop products for treating conditions in which cyclic nucleotide pathways are aberrant and for modulation of intracellular cyclic nucleotide levels. The PDE8 polypeptides exhibit high affinity for hydrolysis of both cAMP and cGMP but relatively low sensitivity to enzyme inhibitors specific for other PDE families. The PDE8A polypeptides and polynucleotides can be used for identifying their specific binding partners. The products can provide approaches for treating conditions in which cyclic nucleotide pathways are aberrant as well as conditions in which modulation of intracellular cAMP and/or cGMP levels in certain cell types is desirable

Sequence 4389 BP; 1315 A; 922 C; 920 G; 1232 T; 0 U; 0 Other;

Query Match 51.9%; Score 1871.8; DB 2; Length 4389;  
 Best Local Similarity 86.5%; Pred. No. 0;  
 Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

415 CTTCCCTTCGCAACGCTTGGCCGCTCGCTCGGCTCGCATGGAAGATGACCTC 474  
 2 CTTGCGCTCGCGCGCGCGCGCGCTGCTCTTGGCTCGCATGGAAGATGACCTC 61  
 475 TAAACAATGCGAAGTTGCTTCCGAAGCTGACCGAGTCTTCTCCAGCCCACTTGA 534  
 62 TAAATAATGCGAAGTCTTCCGAAGCTGACCGAGTCTTCTCCAGCCCACTTGA 121  
 535 TGAAGAAGTGAAGGCTTATCTTCTCCATCCCAAGATTTGATGAATTTGTTCTGA 594  
 122 TGAAGAAGTGAAGGCTTATCTTCTCCATCCCAAGATTTGATGAATTTGTTCTGA 181  
 595 AAGTGTATGTCAGAGACCTGTGAAAGTGGCTGAAGAGAAACAACAAGCAAAAG 654  
 182 AAGTGTATGTCAGAGACCTGTGAAAGTGGCTGAAGAGAAACAACAAGCAAAAG 241  
 655 TGAACCATCTCCCAAGAAAGTCAAGAGTACAGAGATACAGATATGCAAGGATCGTGA 714  
 242 TGAATGCGCTCTTAAGAGATGACAGAGTACAGAGATACAGATATGCAAGGATCGTGA 301  
 715 CGAGCTGAACAGCTACATAGAGACGCGCTGACACGCGCGGGACAACAACCTGCTCT 774  
 302 TGAACCTAACAAGCTATATAGAACACGCTTGACACAGAGAGACAACAACGCTACTCT 361  
 775 CTATGAGCTCAGACGATCATCAGATAGCCACAAAACCGACGATTTGCACTGTAAT 834  
 362 CTATGAGCTCAGACGATCATTAAATAGCCACAAAACCGATGAGATTTGCACTGTAAT 421  
 835 CTTTGAAGTGAATTAATGCGCTGTGTGTTCAATCAACCGGAGATGAAGAGGCCA 894  
 422 CTTTGAAGTGAATTAATGCGCTGTGTGTTCAATCAACCGGAGATGAAGAGGCCA 481  
 895 ACCCGGCTCATCTCTGACAGGCGCCATACCCAGGATACCAATCTCTGCTTACGTCG 954  
 482 ACCCGGCTCATCTCTGACAGGCGCCATACCCAGGAGACAACCGCTCTTATATGTCG 541  
 955 CAAGCTTGAAGAGAGCTTTGTTGTAAGAGATATCTTGGGAGATGAGGATTTCTCGAG 1014  
 542 CAAGTCAAGAGAAACACTGCTATGTAAGACATCTCTTGAAGATGAAGATTTCCAAAGG 601

QY 1015 TACTGCGCTGGAATCAGGAACCCGATCCAGTCTGTTGCTTGGCCCATGTCATCTC 1074  
 DB 602 TACTGCGCTGGAATCAGGAACCCGATCCAGTCTGTTGCTTGGCCCATGTCATCTC 661  
 QY 1075 CATTGGAAGCTTGAATGTCATCTTGAACCTGTACAGGCACTGGGGCAAAAGGCTTCTG 1134  
 DB 662 AATTGGAAGCTTGAATGTCATCTGACCTGTATGCGCACTGGGGCAAAAGGCTTCTG 721  
 QY 1135 CCTCAGCAATCAGAGAGTTGCAACAGCCCAATCTTGGCTTCCGATAGCAATACCA 1194  
 DB 722 TCTTAGTACCAAGAGGTTGCAACAGCAAAATCTTGGCTTCCGATAGCAATACCA 781  
 QY 1195 GGTGAGGTTGTAAGGTTCTGCGCAACAGCCGAATGATGACTTCTACTGACGT 1254  
 DB 782 GGTGAGGTTGTAAGGTTCTGCGCAACAGCCGAATGATGACTTCTACTGACGT 841  
 QY 1255 ATCAAGACATATCTTGAATACATAGTTGCCATAGACTCTCTTAATTGAACATCATAT 1314  
 DB 842 ATCAAGACATATCTTGAATACATAGTTGCCATAGACTCTCTTAATTGAACATCATAT 901  
 QY 1315 ATATGCAAAAAATCTAGTGAACCGGACCGCTGCGCTCTCCAGTGGACCAAGAA 1374  
 DB 902 ATATGCAAAAAATCTAGTGAACCGGATCGATGCTGTGCACTTTCAGAGTGAACCAATGA 961  
 QY 1375 CAAGAGCTGTACTGGAACCTGTTGACATTTGGGAGAGAGAGGAGCCCATCTT 1434  
 DB 962 CAAGAGCTGTACTGGAACCTTGTGATATGGAAGGAGAGAGAGAGAGAGAGAGAG 1021  
 QY 1435 CAAGAGACCAAGAGATCAGATATTTCCATTGAGAAAGGATTTGCTGATCAAGTGGCAAG 1494  
 DB 1022 CAAGAGACCAAGAGATCAGATATTTCCATTGAGAAAGGATTTGCTGATCAAGTGGCAAG 1081  
 QY 1495 AACAGGCGAAGTCTTGAACATTTCCGATCCGATCCGACCTCTGTTTAAACAGGAGGT 1554  
 DB 1082 AACAGGCGAAGTCTTGAACATTTCCGATCCGATCCGATCCGATCCGATCCGATCCG 1141  
 QY 1555 GGAACCTGTACAGGCTTACCAAGAGAAACATTCGTGTATGGCCATAGTGAGCCGAG 1614  
 DB 1142 AGACTTGTACAGGCTTACCAAGAGAAACCTGTGTATGGCCATAGTGAGCCGAG 1201  
 QY 1615 CAGCGTGAATGCGGTGTCAGATGTTGAAACAGATCAGCGGTGAGCGCTTCTCAAGAC 1674  
 DB 1202 CAGCGTGAATGCGGTGTCAGATGTTGAAACAGATCAGCGGTGAGCGCTTCTCAAGAC 1261  
 QY 1675 AGACGAGAACATCTCAAGATTTGCTGCTTCTGCGCATGCGCTTGTGACATGTCCTA 1734  
 DB 1262 AGACGAGAACATCTCAAGATTTGCTGCTTCTGCGCATGCGCTTGTGACATGTCCTA 1321  
 QY 1735 CATGTACCAAGATTCGCGCATCTCAGAAATGCAATCTACAGGTTTACATGAGAGAGCTTC 1794  
 DB 1322 CATGTACCAAGATTCGCGCATCTCAGAAATGCAATCTACAGGTTTACATGAGAGAGCTTC 1381  
 QY 1795 CTACCAACAGATCTGCAACCTCCAGAGTGGCAAGGCTCATGCGCTTCAACCTTACAG 1854  
 DB 1382 CTACCAACAGATCTGCAACCTCCAGAGTGGCAAGGCTCATGCGCTTCAACCTTACAG 1441  
 QY 1855 ACSCATCTGCGCGGACATCAGAGCTATTCATCTTGAATTTGCTTGTGAGAACATGTC 1914  
 DB 1442 GCCTCTCTGCAAAAGAAATTTGAATTTATTCATCTTGAATTTGCTTGTGAGAACATGTC 1501  
 QY 1915 GCCTGGAATCTTGTCTACATGATTCATGCTTGTGAGAACATTTGCTTGTGAGAACATTTGA 1974  
 DB 1502 GCCTGGAATCTTGTCTACATGATTCATGCTTGTGAGAACATTTGCTTGTGAGAACATTTGA 1561  
 QY 1975 AAAATTTGCGCTTTTATCATGCTGTGAGAAAGAACTATCGCGGAGTTCTTACACCA 2034  
 DB 1562 AAAATTTGCGCTTTTATCATGCTGTGAGAAAGAACTATCGCGGAGTTCTTACACCA 1621  
 QY 2035 CTGGAAGCATGCAAGTACGAGTGGCAACATGCTGATATGCTTCAAAACCAACATGAG 2094  
 DB 1622 CTGGAAGCATGCAAGTACGAGTGGCAACATGCTGATATGCTTCAAAACCAACATGAG 1681  
 QY 2095 CTTCTTCAACAGACCTGAGCGCAAGGCTGCTTAATTTGCTGTCTGTGCAATGACCTGGA 2154

Db	1682	GCTTTTCACAGACCTT	AGCGCAAGGAC	TGCTGATTCGCTGTCATGAC	CTTGGAA	1741	
Qy	2155	CCACAGGGGGCTT	CAGTAA	CAGCTACCTC	CAGAAAGTTTCAGCACCCCTTGCGGCGCTGTA	221.4	
Db	1742	CCACAGGGGGCTT	CAGTAA	CAGCTACCTC	CAGAAAGTTTCAGCACCCCTTGCGGCGCTCTTA	1801	
Qy	2215	CTCCACCTT	CCACATGAG	CAACACACTT	CTCCAGACGGTGTCCATCTTCACTGGA	227.4	
Db	1802	CTCCACCTT	CCACATGAG	CAACACACTT	CTCCAGACGGTGTCCATCTTCACTGGA	1861	
Qy	2275	AGGGGACAAATAT	CTTCTT	CCACCTT	CCAGCGAGTACAGACAGAGGTGCTGGAGATCAT	233.3	
Db	1862	AGGGGACAAATAT	CTTCTT	CCACCTT	CCAGCGAGTACAGACAGAGGTGCTGGAGATCAT	1921	
Qy	2335	CGGCAAAACCAT	CATCGC	CACCGA	CCTCGCCTTAATCTTTGGGAA	CAGGAAAGCACTTGGAA	239.4
Db	1922	CGGCAAAACCAT	CATCGC	CACCGA	CCTCGCCTTAATCTTTGGGAA	CAGGAAAGCACTTGGAA	1981
Qy	2395	GGAGATGTAC	CAGACAGAGG	TCGCTGA	ACCTCCACACAGCTCCATCGAGACCGTGTCA	245.4	
Db	1982	GGAGATGTAC	CAGACCGGAT	CACTAAACCTTA	TATCATCATCATAGAGACCGTGTAT	204.4	
Qy	2455	CGGCTTGAATGAT	GATCTGCT	GTGATCTT	TGCTGTGACCAAACTATATGGCCAGTTACAA	251.4	
Db	2042	TGGTTTGAATGAT	GATCTGCT	GTGATCTT	TGCTGTGACCAAACTGTGGCCCGTTACAA	2101	
Qy	2515	ATTGACAGGAA	TGATATATATATG	CAGAAATTTCTGGGCTGAGGGTGA	TGAGATGAAGAAGCT	257.4	
Db	2102	ATTGACGCAAA	TGATATATATATG	CAGAAATTTCTGGGCTGAGGGTGA	TGAAATGAAGAAAT	2161	
Qy	2575	GGGCAATACAG	CCCATCTT	CTATGATGGA	CAGACACAGACGAGATGAAGTCCCTCAAGGGCA	263.4	
Db	2162	GGGAATACAG	CCCTATTTCT	TATGATGGA	CAGACACAAAGATGAAGTCCCCAAGGCCA	2221	
Qy	2635	GCTCGGATTT	CTACAA	TGCTGTG	GGCAATTCCTGTCTATACACACTTGAAGCAGATCTCTCC	269.4	
Db	2222	GCTTGGGTTT	CTACAA	TGCTGTG	GGCAATTCCTGTCTATACACACTTGAAGCAGATCTCTCC	2281	
Qy	2695	ACCCACAGAG	CCCTCGTGA	AGGGCC	TGACAGGGATTAACCTCAATCAGTGGGAGAAAGTAA	275.4	
Db	2282	TCCCAACGAG	CCCTCTTCTGA	AAAGCATG	CAGGGATATATCTCACTCAGTGGGAGAAAGTAA	2341	
Qy	2755	TCGCGGGAG	AGAGACAGCAAT	TGTGATTT	CAGGCC	CAGGCGCGGCGC	2801
Db	2342	TCGAGGGAG	AGAGACTGCA	CTGGAATTTCA	TCCCAATCCGATCCGATGCTC	2388	
RESULT 12							
AAC63696							
ID	AAC63696 standard, cDNA, 4389 BP.						
XX	AAC63696;						
AC	.						
DT	13-FEB-2001 (first entry)						
XX	Human phosphodiesterase 8A1 PDE8A1 coding sequence.						
DE	Human, PDE8A1, phosphodiesterase 8A1, chromosome 6p26-27, 88.						
XX	Homo sapiens.						
OS	Homo sapiens.						
XX	US6133007-A.						
PN	17-OCT-2000.						
XX	16-OCT-1998;						
PF	98US-00174437.						
XX	16-OCT-1997;						
PR	97US-00951648.						
XX	(ICOS-) ICOS CORP.						
PA	Loughney K,						
XX	PI						

XX	WPI: 2001-006138/01.
DR	P-PSDB; AAB28257.
XX	New phosphodiesterase 8A (PDE8A) polypeptides useful used in the
PT	systematic analysis of the structure and function of PDE8, and for
PT	identifying molecules with which PDE8A will interact.
XX	
XX	Example 3; Col 31-40; 37pp; English.
PS	
XX	The present sequence is the coding sequence for human phosphodiesterase
CC	8A1 (PDE8A1). Phosphodiesterases hydrolyse 3', 5' cyclic nucleotides to
CC	their respective nucleoside 5' monophosphates. The present sequence is a
CC	splice variant of PDE8 (AAC6395). This sequence may be used in the
CC	systematic analysis of the structure and function of PDE8, and for the
CC	identification of molecules with which PDE8 will interact. The present
CC	sequence may be used in hybridisation assays to detect the capacity of
CC	cells to express PDE8, and as a basis for diagnostic methods useful for
CC	identifying a genetic alteration in a PDE8 locus that underlies a disease
CC	state or states. The human PDE8 gene has been localised to chromosome
CC	6p26-27
SQ	Sequence 4389 BP; 1315 A; 922 C; 920 G; 1232 T; 0 U; 0 Other;
Query Match	51.9%; Score 1871.8; DB 4; Length 4389;
Best Local Similarity	86.5%; Pred. No. 0; Mismatches 322; Indels 0; Gaps 0;
Matches 2065; Conservative	0;
OY	CTTCCCCCTTCACACCGTTTGCGCGCTGCCCTTCGCGCTCGACATGGAATGAGCCTC 474
Db	2 CTTCGCCCTCGCGCGCGCGCGCGCGCGCGCGCTTCCTTGCGCTCGACATGGAATGAGCCTTC 61
OY	475 TTAACATGCGAGTTGTCTTCGAGAGCTGCACCAGATGTTTTCTCAAGCCCCCATGTTGACGGA 534
Db	62 TAAATATGCGAGCTGGCTTCGAGAGCTGCACCAGATGTTCTTGAGCCCATGTTGACGAGA 121
OY	535 TGAAAAGGTGAAGGCTTACTTTCTCTTCATCCCAGATTAATGATATTGTTCTCGA 594
Db	122 TGAATAAGGTGAAGGCAATCTTCTCTCTCAACCCCAAGTATTAATGATTTGATCTGA 181
OY	595 AAGGTATAGTCAGACGCTGNGAAGTAGTGCTGAAGAGAAACAACAAAGCAAAGA 654
Db	182 AAGGTATAGTCAGACGCTGNGAAGTAGTGCTGAAGAGAAACAACAAATTCAGAGA 241
OY	655 TGAACCATCTCCCAAGAGAGTCAGACAGGTACAGAGATACGAATATGACGGAGTCGTETA 714
Db	242 TGAATCGGCTCTTAAGAGAGTCAGACAGGTACCAAGATACGAATATGACGGAGTTGATTA 301
OY	715 CGAGCTGAACAGCTCATATAGACACGCCCTTGACACGGGCGGGACAACACCTGCTCT 774
Db	302 TGAATCAAAAGCTATATATAGAACAAAGCTTGACACAGAGAGAACAAACAGCTACTCT 361
OY	775 CTATAGAGCTCAGACGATCATCAGAGTAGCCACAAAAAGCGAGATTGCACTGTACTT 834
Db	362 CTATAGAGCTCAGACGATCATTTAAATAGCCACAAAGCCAGATTTGCACTGTATTT 421
OY	835 CCTTGAGAGTGCAATATATAGCCTGTGTGTTCATACCAACCGGAGTGAAGAGAGCCA 894
Db	422 CCTTGAGAGTGCAATATATAGCCTGTGTATATTCACGCACTGGGATTAAGAGAGAGAA 481
OY	895 ACCCGGCTCATCCCTGCGAGGGCCCATCACCAAGGATACACATCTTGCTTACGTGTC 954
Db	482 ACCCGGCTCATCCCTGCTGGGCCCATCACCAAGGACCAACGCTCTGTGTATGTGGC 541
OY	955 CAAGCTATGGAAGACCTTGTGTGTATGAGGATATCTTGGGGATAGAGGATTTCTCGAGS 1014
Db	542 CAAGCTCAGAGAAACACTGCTATGATGAAGATCTTGGAGATGAACATTTTCAAGAGS 601
OY	1015 TACTTGAGCTGGAATCAGAGAACCCCATCATCAGCTCTGTTCTTGCTTGCCATGTCACTGC 1074
Db	602 TACTTGAGCTGGAATCAGAGACTCGATCATCAGCTCTGTTCTTGCTTACCAATGTCACTGC 661
OY	1075 CATTGAGACTTGTGATGTGCACTCTTGAACGTATACAGGACCTGGGGCAAAAGAGCCTTCTG 1134







```
DB 1742 CCAAGGGGGCTTCAGTAACAGTACCTGAGAGTTGACCAACCTCTGGCCGCTCTCTA 1801
OY 2215 CTCGACCTTCACCATGAGAGACACCACTTCTCCAGACGGTGTCCATCTTCAAGCTGGA 2274
DB 1802 CTCGACCTTCACCATGAGAGACACCACTTCTCCAGACGGTGTCCATCTTCAAGTGA 1861
OY 2275 AGGGGCAATATCTTCTCCACCTTGAGCTCCAGCGATGACGAGAGCTGTGAGATCAT 2334
DB 1862 AGGGGCAATATCTTCTCCACCTTGAGCTCCAGTGAATGAGAGCTGTGAGATCAT 1921
OY 2335 CCGCAAGCATCATGCGCAACCGACCTGCGCCCTATCTTTGGGACAGGAACAGTTGGA 2394
DB 1922 CCGCAAGCATCATGCGCAACCGACCTGCTTTATCTTTGAAACAGGAGAGATTGGA 1981
OY 2395 GGAAGATGATCAGACAGGGTCCGTGAACCTCAACAACAGTCCCATCGAGACCGTGTCA 2454
DB 1982 AGAGATGATCAGACCGGATCACTAATCCTTAATATCATCATAGAGACCGTGTAT 2041
OY 2455 CCGCTTGATGATGATGCTGCTGTGATCTTGTCTGTGACCAACATATGCGCAGTTACAA 2514
DB 2042 TGGTTTGATGATGATGCTGCTGTGACCTTTGTCTGTGACAAACATGTGGCCGTTACAA 2101
OY 2515 ATTTGACAGCGAATGATATATATGACGAATTTCTGGGCTGAGGGTGAAGATGAAGAAGT 2574
DB 2102 ATTTGACGCGAATGATATATATGACGAATTTCTGGGCTGAGGGTGAAGATGAAGAAT 2161
OY 2575 GGGGATACAGCCCATCTATGATGACAGAGACAGACGAGATGAAGTCCCTCAAGGCA 2634
DB 2162 GGGAAATACAGCCCTATCTATGATGACAGAGACAGAGAGATGAAGTCCCGCAAGGCA 2221
OY 2635 GCTCGGATTTCTAATGCTGTGTGCGCAATCCCTGCTATACCACTTTGACGCAATCTCTCC 2694
DB 2222 GCTGGGTTCTAACAATGCGGTGCGCAATCCCTGCTATACCACTTTACCAAGATCTCTCC 2281
OY 2695 ACCCAGACAGCTCTGTCTGAGAGCGCTGACAGGATTAACCTTCATCATGAGGAGAAAGTAT 2754
DB 2282 TCCCAAGGAGCGCTCTGTGAGAGCATGACAGGATTAATCTCATGAGTGGAGAAAGTAT 2341
OY 2755 TGGCGGAGAGAGACAGCAATGATGATTTCAAGGCCCAAGGCCCGCGC 2801
DB 2342 TCAGGAGAGAGAGACATGCACTGAGATTTCAATCCCATCCGTGGCTC 2388

RESULT 14
AAA09590
ID AAA09590 standard; cDNA to mRNA; 2406 BP.
XX
AC AAA09590;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human phosphodiesterase 10 (PDE10) nucleotide sequence SEQ ID 2.
XX
KW Phosphodiesterase 10; PDE10; human; ss.
XX
OS Homo sapiens.
XX
PN JP2000224992-A.
XX
PD 15-AUG-2000.
XX
PF 11-MAY-1999; 99JP-00129343.
XX
PR 30-NOV-1998; 98JP-00338861.
XX
PA (TANA ) TANABE SEIYAKU CO.
XX
WI WI; 2000-605129/58.
XX
DR P-PSDB; AAB26854.
XX
PT Novel phosphodiesterase and its gene for research on complex mechanism of intracellular information transfer.
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XX
PS Claim 2; Page 16-19; 29pp; Japanese.
CC Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
XX proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful
CC for research on the complex mechanism of intracellular information
CC transfer. The invention includes a recombinant vector containing a PDE10
CC gene, and a cell transformed with the vector. Sequences AAA09593-A09606
CC represent PCR primers used in the isolation of the PDE10 polynucleotide
XX sequences of the invention
SQ Sequence 2406 BP; 692 A; 551 C; 562 G; 601 T; 0 U; 0 Other;
Query Match 51.7%; Score 1864.2; DB 3; Length 2406;
Best Local Similarity 86.9%; Pred. No. 0; Mismatches 308; Indels 0; Gaps 0;
Matches 2049; Conservative 0;
OY 445 CTTGGGCTCCGACATGAGAGATGACCTCTTAACATGCGAGTTGCTTCCGAGGCTGAC 504
DB 2 CTTGGGCTCCGACATGAGAGATGAGCTCTTAATATGCGAGCTGCTCCGAGGCTGAC 61
OY 505 CGAGTGTCTCTCAGCCCCAGTTTGAACGATGAGAAAGGTGAAGGCTATCTTCTCCA 564
DB 62 CGAGTGTCTCTCAGCCCCAGTTTGAACGATGAGAAAGGTGAAGGCAATCTTCTCTTGA 121
OY 565 TCCCGAGGATTAATGATGATTTGTTCTGAAGGTGTTAGTGACAGACTGTGAAAAGTG 624
DB 122 CCCCCAGGATTAATGATGATTTGTTCTGAAGGTGTTAGTGACAGACGTAAGAAATG 181
OY 625 GCTGAAGAGAGAAACCAACAAAGAGATGAACCATCTCCCAAGAGATGACAGGTA 684
DB 182 GCTGAAGAGAGAAACCAACAAATCAGAAATGAAATCAAGCTCTTAAGAGATGACAGGTA 241
OY 685 CCAGATTAAGATATGACAGAGAGTGTGTAAGAGTGAACAGCTTACATGACAGGCT 744
DB 242 CCAAGATTAAGATATGACAGAGAGTGTGTAATGAATGAACAGCTATATGAACAACGCTT 301
OY 745 GGAACAGGCGGGGACAAACCACTGCTCTATAGAGCTCAGACATCATCAGATAGC 804
DB 302 GGAACAGAGAGAGACAAACCACTCTCTATGAACAGACATCATTAATTAATAGC 361
OY 805 CACAAAAGCCGACGAGATTTGACATGATCTCTTGAGAGATGCAATATATAGCTGTGT 864
DB 362 CACAAAAGCCGATGATTTGACATGATTTCTTGAGAGATGCAATATATAGCTGTGT 421
OY 865 GTTCATACCAACCGGATGAGAGAAAGCCCAACCCGCTCATTCCTGCAAGGCCATAC 924
DB 422 ATTCACGCAACCGGATTAAGAGAGAAACCCGCTCATTCCTGCTGGGCCATAC 481
OY 925 CAGGGTACCAACCATCTTCTGCTGAGTGGCCAAAGTATAGAGAACCTTGTGTAGAGA 984
DB 482 TCAGGCAACCAACCGTCTGCTTATGTGGCAAGTCCAGAAAACACTCTGTATAGAGA 541
OY 985 TATCCTTGGGATGAGAGATTTCTGAGAGTACTGGCTGGAATCAGAACCCGATCCA 1044
DB 542 CATCTTGAGATGAGAGATTTCTGAGAGTACTGGAATCAGAACCTGATCCA 601
OY 1045 GTCTGTTCTTTGCTTGCCCATTTGTCACTGCACTTGAGACTTGATTTGCAATCTTGA 1104
DB 602 GTCTGTTCTTTGCTTTCATTAATGTCACTGCAATTTGTGATTTGATTTCTCGAGCT 661
OY 1105 GTACAGGCACTGGGGGAAAGAGGCTTTGTGCTCAGCCATCAGAGAGTTGCAACAGCA 1164
DB 662 GTATCGGCACTGGGGGAAAGAGGCTTTGTGCTTATGTACACAGAGAGTTGCAACAGCA 721
OY 1165 TCTTGCTTGGGCTTCCGTAGCAATACACAGGAGTGAAGTGTGAGAGTCTCGCAACA 1224
DB 722 TCTTGCTTGGGCTTCCGTAGCAATACATCAGGAGTGAAGTGTGAGAGTCTCGCAACA 781
OY 1225 GACGAACTGAATGATCTTCTACTGACGATCAAAAGACATTTGATTAATATAGTTGC 1284
DB 782 GACGAAATGAATGATCTTCTACTGACGATCAAAACATATTTGATTAATATAGTTGC 841
```

OY	1285	CATGAGCTCTCTACTTTGAAACAATCATGATATATATGCCAAAATAATCTAGTGAAGCGCGACCG	1344
Db	842	AATGATATCTCTACTTTGAAACAATCATATATATATATGCAAAAAAACCCTGCTGAATGCCAGTCG	901
OY	1345	CTGCGCGCTCTTCCAGGTGGGACCAACAAGAACAGAGGCTGTACTCGACCTGTTTGACAT	1404
Db	902	TTGTGCGCTTTTCCAGGTGGACCAATAGAACAGAGGATTATATTCAGACCTTTTGGATAT	961
OY	1405	TGGGAGGAGAAAGAGGGGAAAGCCCATCTTCAAGAGACCAAGAGATCAGATTTTCCAT	1464
Db	962	TGGAGAGGAAAGAAAGGAAAAAACCCTGTCTTCAAGAAAGACCAAAAGAGATTAATTTTCAAT	1021
OY	1465	TGAGAAAGGATGTGCTGTCAAGTGGCAAGAACAGGCCAATCTTTGAACATTTCCGATGC	1524
Db	1022	TGAGAAAGAAATGTGCTGGCCAAAGTAGAAGAACAGGGGAAGCTCTGAACATTTCCAGATGC	1081
OY	1525	CTACGCGGACCCCTCGCTTTTAAACAGGAGAGTGGACCTGTATACAAGGCTACACAGAGGA	1584
Db	1082	CTATGCAAGACCCACGCTTTTAAACAGAAAGTAGACTTTATACAGGCTACACACGGGAA	1141
OY	1585	CATTCTGTGTATGCCCATAGTGAAGCCGAGGACGCGTGAATGGCGTGTGCAGATGGTGA	1644
Db	1142	CATCCTGTGATGATGCCCATGTGTCAGCCGAGGAGCGGTGATGAGTGTTGGCAGATGGTCAA	1201
OY	1645	CAAGATCAGCGGTAGCGGCTTCTCCAAACAGACGAGAAACAACCTTCAAGATGTTTGTCTGT	1704
Db	1202	CAAATATAGTGGCAGATGCGCTTCTCTAAACAGATATAAAACAATTCAAAATGTTTGGCGGT	1261
OY	1705	CTTCTGCGCACCTGGCTTGCACTGTGCTTAAACATGTATACCAGAGATCCGCGCACTCGAATG	1764
Db	1262	CTTTTGTGCTTTAGCCTTATACATGTGTCTAATATATATATATAGTAATTCGCACTCAGAGTG	1321
OY	1765	CATCTACAGGGTTACCATGAGAAAGCTTTCCTACACAGCATCTGCACCTCCAGAGAGTG	1824
Db	1322	CATTATACGGGGTAATGAGATGAAAGACTGTGCTTACCATATAGCAATTGTGTACTTCAGAAAGAGTG	1381
OY	1825	GCAAGGCTCATGTGCAATTCACACCTTCCCGTGTCTTCGCAAAAGAAATGGAATTAATTCGA	1441
Db	1382	GCAAGGCTCATGTGCAATTCACACCTTCCCGTGTCTTCGCAAAAGAAATGGAATTAATTCGA	1441
OY	1885	CTTTGACATTTGGTCCCTTTGAGAAACATGTGGCTGGAGATCTTTGTCTACATGATGCATCG	1944
Db	1442	CTTTGACATTTGGTCCCTTTTGAAGAAATGTGGCTGGAGATTTTGTCTACATGATGCATCG	1501
OY	1945	GTCTTGTGGGACATCTCTGTTTTTGAACCTTGAAGAAATTTGGCGTTTATCATGTCTGTGA	2004
Db	1502	GTCTCTGTGGGACATCTCTGCTTTGAGCTTGAAGAAATGTGTGTGTTTATATATGTCTGTGA	1561
OY	2005	GAAAGAACTATGGCGGGTTCCTTACCAACATGGAAGCATGCAAGTCAACGCTGGCACTGTG	2064
Db	1562	GAAAGAACTATGGCGGGTTCCTTATCAACAATGGAAGCATGCGGTCACTGTAGCACTGTG	1621
OY	2065	CATGATATGCCATCTTTCAAAACAACAATGGCCTCTTCAACAGCCTCGAGCGCAAAAGGCT	2124
Db	1622	CATGATATGCCATCTTTCAGAACAAATCAACGCTTTTCAACAGCCTTGAAGCGCAAGAGACT	1681
OY	2125	GCTAATTCGCTGTCTGTGCAATGACCTTGAACAACAGGGCTTCACTGAACAGCTATCTTGA	2184
Db	1682	GCTGATTCGCTGTCTGTGCAATGACCTTGAACAACAGGGGCTTCACTGAACAGCTATCTTGA	1741
OY	2185	GAAAGTTGCAACCAACCCCTGGCGGGCGCTGTATCTCAACTTCACCATGAGCAACACACTT	2244
Db	1742	GAAAGTTGCAACCAACCCCTGGCGCGCTCTCTAATCTCAACTTCACCATGAGAGCAACACTT	1801
OY	2245	CTCCCAAGCGGTGTCCATCTTCAACCTGGAAGGGGCAAAATCTTCTCAACCTGAGAGTC	2304
Db	1802	CTCCCAAGCTGTGTCCATCTTCAAGTTGAAGGGGCAAAATCTTCTCAACTCTGAGAGTC	1861
OY	2305	CAGCAGATACGAGCAGGTGCTGGAATCATCGCAAAACCAATCATCGGCCACCGCACTTGC	2364
Db	1862	CAGTGAATATAGCAGGTGCTTGAATCATTCGCAAAACCAATCATTCGCCACAGACCTTGC	1921
OY	2365	CCTAATCTTTGGGAAACAGAAACAGTTGGAAGATGTATCCAGACAGGCTGCTGAACCT	2424

Dd		1922	TTTATACCTTTGGAAAACAAGAAAGCATTGGAAGAATGTACCAAGCCGATCACATAAACC	1981
Oy		2425	CCACAACCAAGTCGCCCATCGAGACCGGTGCATCGCCTTAGATGAATCGCTGTGATCTTTG	2484
Dd		1982	TAAATATCAATCACAATAGAGACCGTGTAATTGGTTGATGATGACTGCGCTGTGACCTTTG	2041
Oy		2485	CTCTGTGACCAAACTATATGCGCCAGTTTACAAAAATTCACAGCCGAATGATATATATGACAATT	2544
Dd		2042	TTCTGTGACAAACTGTGGCCCCGTTACAAAATTGACGGCAATATATATATGACAAATT	2101
Oy		2545	CTGGGCTGAGGGTATGATGATGAAGAAGCTGGCATACAGCCCAATTCCTATGATGACAG	2604
Dd		2102	CTGGGCTGAGGGTATGATGAATGAAGAAATTGGAAATACAGCTATTCCTATGATGACAG	2161
Oy		2605	AGACAAGCGAAGTGAAGTCCCTCAAGGGCAGCTCGAATTTACAAATGTGTGCCCATTC	2664
Dd		2162	AGACAAGAAGATGAAGTCCCCCAAAGGCAGACTTGGGTTTACAAATGCGTGGCCATTC	2221
Oy		2665	CTGCTATATCCACCTTTGACGACGATCTTCCACCCACAGAGCCTTGTCTGAAGCCTGCAG	2724
Dd		2222	CTGCTATATCAACCTTTTACCCAGATCTCCCTCCACGAGCCTCTTCTGAAGCATGCA	2281
Oy		2725	GGAATACCTCAATCAGTGGGAGAGATTAATCGCGGGAGAGACAGACAATGTGGATTTC	2784
Dd		2282	GGAATATCTCAGTCAGTGGGAGAGAGTATTGAGGGAGAGACTGCACACTGGATTTC	2341
Oy		2785	AGGCCCAAGGCCCGCGC	2801
Dd		2342	ATCCCACATCGGTGGCTC	2358
<b>RESULT 15</b>				
AAdZ36963	ID	AAdZ36963	standard; DNA; 2554 BP.	
XX AC	AAZ36963;			
XX DT	13-MAR-2000	(first entry)		
XX DE	DNA encoding a human phosphodiesterase enzyme designated PDE11A1.			
XX Km	Phosphodiesterase enzyme; PDE11A1; PDE11A2; splice variant; PDE11; cGMP;			
XX Km	GMP; male erectile process; sexual dysfunction; PDE11 imbalance; ss.			
XX OS	Homo sapiens.			
XX FH				
XX Key		Location/Qualifiers		
FT CDS		13..2382		
FT FT		/*tag= a		
FT FT		/product= "phosphodiesterase enzyme"		
XX PN	EP967284-A1.			
XX PD	29-DEC-1999.			
XX PF	21-MAY-1999;	99EP-00303985.		
PR PR	28-MAY-1998;	98GB-00011500.		
PR PR	30-OCT-1998;	98GB-00023882.		
PR PR	04-DEC-1998;	98GB-00026777.		
PR PR	09-APR-1999;	99GB-00008247.		
PR PR	10-MAY-1999;	99GB-00010801.		
PA PA	(PFIZ ) PFIZER LTD.			
PI PI	(PFIZ ) PFIZER INC.			
XX Lanfear J,	Robas NM;			
XX WPI;	2000-064614/06.			
DR P-PSDB;	AAV53935.			
XX Novel polypeptides	and polynucleotides used to identify agents which			





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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 02:12:24 ; Search time 13496 Seconds  
(without alignments)  
12501.054 Million cell updates/sec

Title: US-10-618-252-14  
Perfect score: 3606  
Sequence: 1 acgcgtccgcctccatctg.....aatttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_ests1:  
2: gb\_ests2:  
3: gb\_ests3:  
4: gb\_ests4:  
5: gb\_ests5:  
6: gb\_ests6:  
7: gb\_ests7:  
8: gb\_ests8:  
9: gb\_ests9:  
10: gb\_ests10:  
11: gb\_ests11:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3066	85.0	3611	4 AK039249	AK039249 Mus muscu
2	1703.2	47.2	2340	11 DQ048769	DQ048769 Homo sapi
3	1596.6	44.3	2237	11 DQ048770	DQ048770 Pan trogl
4	797.8	22.1	820	8 CX241410	CX241410 NMA04348
5	759.8	21.1	836	8 CX562742	CX562742 UI-M-IBO-
6	755.2	20.9	772	6 CD805436	CD805436 UI-M-GMO-
7	752	20.9	755	6 CB243359	CB243359 UI-M-FYO-
8	720.8	20.0	736	6 CB245079	CB245079 UI-M-FYO-
9	720.8	20.0	861	6 CX238886	CX238886 NMA06506
10	690.2	19.1	702	6 CP182788	CP182788 UI-M-EYO-
11	681.4	18.9	683	7 CP913876	CP913876 B0955F07-
12	677.8	18.8	681	7 CP913322	CP913322 B0933E08-
13	671	18.6	671	3 BM230520	BM230520 K0296G04-
14	670.2	18.6	680	6 CF725825	CF725825 UI-M-GZO-
15	646.4	17.9	662	8 CX241102	CX241102 NMA03974
16	645	17.9	645	3 BM228841	BM228841 K0268H06-
17	632.2	17.5	829	8 CX782297	CX782297 HES03_13
18	605.8	16.8	815	7 CK597964	CK597964 AGENCOURT
19	588.8	16.3	694	5 BY720061	BY720061 Mus muscu
20	586.2	16.3	784	4 AK014090	AK014090 Mus muscu
21	586.2	16.3	1012	5 BY713085	BY713085 BY713085
22	555.4	15.4	840	7 CK595176	CK595176 AGENCOURT

23	553	15.3	553	2 BE861486	BE861486 UI-M-API-
24	546.2	15.1	570	1 AT508642	AT508642 vb54e11.Y
25	537	14.9	636	5 BY723598	BY723598 BY723598
26	534.4	14.8	824	8 CX925624	CX925624 JGI CAAN1
27	528.4	14.7	782	1 AU120086	AU120086 AU120086
28	525.4	14.6	527	7 CN679364	CN679364 E0123E09-
29	523.8	14.5	527	6 CA888664	CA888664 B0147F11-
30	516	14.3	516	6 CA888663	CA888663 B0147F11-
31	512	14.2	512	6 CA560184	CA560184 K0268H06-
32	511	14.2	514	6 BY475571	BY475571 BY475571
33	509.6	14.1	517	5 BX527582	BX527582 BX527582
34	507.2	14.1	512	5 BU700347	BU700347 UI-M-DJ1-
35	507.2	14.1	670	5 BU524872	BU524872 AGENCOURT
36	500.8	13.9	830	5 BU524872	BU524872 AGENCOURT
37	479.8	13.3	483	6 CA893003	CA893003 B0176A12-
38	476.6	13.2	759	5 BU364111	BU364111 AGENCOURT
39	475.6	13.2	816	5 BQ432728	BQ432728 C0235C01-
40	475.4	13.2	477	6 CA536503	CA536503 vb54e11.Y
41	469.2	13.0	477	1 AA386789	AA386789 602322019
42	466	12.9	987	2 BG171485	BG171485 602322019
43	465.8	12.9	791	1 AU080349	AU080349 AU080349
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## ALIGNMENTS

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LOCUS  
DEFINITION  
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enriched library, clone:A33007F15 product:phosphodiesterase 10A,  
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ACCESSION  
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VERSION  
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SOURCE  
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Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
10349636  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
11042159  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
11076861  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Komno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tachiro, H., Itoh, M.,  
Sumi, N., Iehli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384 format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
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The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
The FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE Group Phase I & II Team.  
 ANALYSIS of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3611)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T.,  
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 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnato, N.,  
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 Sano, H., Sasagaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M., and Hayashizaki, Y.  
 COMMENT Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 CDNA library was prepared and sequenced in Mouse Genome  
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 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
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REFERENCE  
AUTHORS  
1 (bases 1 to 2340)  
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees  
(et) Plos Biol. 3 (6), E170 (2005)

JOURNAL  
PUBMED  
15869325  
2 (bases 1 to 2340)  
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

COMMENT  
JOURNAL  
PUBMED  
15869325  
2 (bases 1 to 2340)  
Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

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SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE AUTHORS Hubisz, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeillio, D., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees  
JOURNAL PLoS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE AUTHORS Hubisz, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeillio, D., White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of

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 Db 1958 ACCGTGTATGAGGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2017

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 CX241410  
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 VERSION CX241410  
 ACCESSION CX241410  
 KEYWORDS CX241410.1 GI:56896702  
 SOURCE  
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 REFERENCE 1 (bases 1 to 820)  
 AUTHORS Williams, C., Witta, W., Wikstrom, L., Lundberg, J. and Pilsen, J.  
 TITLE Expressed sequence tags of cDNA clones from Mus Musculus Lateral Ventricle Wall  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Erlendsson, R.  
 Target Identification  
 NeuroNova AB  
 Flakartorpsvagen 15A-D, S-11433 Stockholm, Sweden  
 Tel: +46 8 786 0915  
 Fax: +46 8 786 0911  
 Email: rikard.erlndsson@neuronova.com  
 Seq primer: M13FWD.  
  
 FEATURES  
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 location/qualifiers  
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ORIGIN  
 Query Match 22.1%; Score 797.8; DB 8; Length 820;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-189;  
 Matches 813; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
  
 Qy 2753 ATTGCGGGGGAAGAGACAGCAATGTGATTTCAAGCCAGGCGCGGCTTGAAGAAGC 2812  
 Db 1 ATTGCGGGGGAAGAGACAGCAATGTGATTTCAAGCCAGGCGCGGCTTGAAGAAGC 60  
 Qy 2813 ACACTGAGAAAGCTGAACGTGAAGATTGAAGACTGATCTGAAGTGAAGTCTGATGTC 2872

Db	61	ACACCTGAGAGCTGAACTGTAAGTGAAGACTGATCTCTGAAGTCTCTGATGCT	120
Qy	2873	GCCGACGAAACCGACTCAACCTGCTCTGAGACTTCTTTTGTTCATGAGGGGTGA	2932
Db	121	GCCGACGAAACCGACTCAACCTGCTCTGAGACTTCTTTTGTTCATGAGGGGTGA	180
Qy	2933	AAACCCCTGTCAGAAAGTACCGTCCGATATTCATGTAAGACGACGCTCCCTGCTG	2992
Db	181	AAACCCCTGTCAGAAAGTACCGTCCGATATTCATGTAAGACGACGCTCCCTGCTG	240
Qy	2993	GACACACCTCGGACAGTGAAGAACCCAGGCTCTGCGGATTCAGACGCTGAGTCTCCG	3052
Db	241	GACACACCTCGGACAGTGAAGAACCCAGGCTCTGCGGATTCAGACGCTGAGTCTCCG	300
Qy	3053	TGGCTTCCACCTGACCTCCGAAATGCTATTTGCTCCAGGACGACGCTGCTGAGAG	3112
Db	301	TGGCTTCCACCTGACCTCCGAAATGCTATTTGCTCCAGGACGACGCTGCTGAGAG	360
Qy	3113	GCGGACAGACCAAGAGAGGTTCTTCTGCTGCACTCTCCATGAGGCTGCGCACTTC	3172
Db	361	GCGGACAGACCAAGAGAGGTTCTTCTGCTGCACTCTCCATGAGGCTGCGCACTTC	420
Qy	3173	CTGGTTCTGTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3232
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Qy	3233	GTGTTGAAGTTTACATGATGACCTTCTTATAGTTTAACTGATGTTGCTGCTGCA	3292
Db	481	GTGTTGAAGTTTACATGATGACCTTCTTATAGTTTAACTGATGTTGCTGCTGCA	540
Qy	3293	GTATATGAGGTCAAGTCTCAAGGTGACAGAGAAATCCAACTGTTGATTACAGTGC	3352
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Db	661	GAAGCATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
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Qy	3533	CTTGGGCACTGCGCAATCCCTTTTATACAAAGAAATAAA	3573
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Qy	663	CTTCCAGAGAACTGACAGCTGACAGTACAGAAATATGAGGAGAGTCTGAGCTGA	722
Db	1	CTTCCAGAGAACTGACAGCTGACAGTACAGAAATATGAGGAGAGTCTGAGCTGA	60
Qy	723	ACAGCTACATAGAGAGAGCTGAGACAGGAGGAGCAACCACTGCTCTTATGAGC	782
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Qy	843	AGTGCATATATAGCTGTGTGTGTTTATACACCCGAGATGAAGAGGCAACCCGAG	902
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Db	191	TCATCCCTGACAGGAGCCATCACCGAGGATGACCACTCTGCTGCTGAGTGA	250
Qy	963	GGAAGAGCTTGTGTGATGAGATATCTTGGGATGAGGATTTCTCTGAGAGTACG	1022
Db	251	GGAAGAGCTTGTGTGATGAGATATCTTGGGATGAGGATTTCTCTGAGAGTACG	310
Qy	1023	TGGAATCAGAAACCCGATCAGTCTGTTCTTCTGCTGCTGCTGCTGCTGCTG	1082
Db	311	TGGAATCAGAAACCCGATCAGTCTGTTCTTCTGCTGCTGCTGCTGCTGCTG	370
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Db	371	ACTGATGAGCACTCTTGAACGTACAGGACCTGAGGAGCAAGAGGCTTCTGCTG	430
Qy	1143	ATCAGAGGTTGCAAGGCAATCTTGTGGCTTCTGCTGCTGCTGCTGCTGCTG	1202
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FEATURES

source

Location/Qualifiers

1..836

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/clone\_id="NIH BMAP 1B0"

/note="Organ: Eye; Vector: pYX-Asc; Site 1: Bcl I; Site 2: Not I; The library was constructed according to Ronald, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AATTAATTAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match

Best Local Similarity 93.9%; Pred. No. 8,2e-180;

Matches 832; Conservative 0; Mismatches 3; Indels 51; Gaps 2;

RESULT 5

CX562742

LOCUS

DEFINITION

IMAGE:6806925 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

EST.

REFERENCE

1 (bases 1 to 836)

NIH-MGC <http://mgc.ncl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa







SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 755)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pyx-5.  
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 site 2: Not I; The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured mRNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not I site. Double stranded  
 cDNA was size selected according to mRNA size fraction,  
 ligated with EcoR I adaptor, digested with Not I, and then  
 cloned directionally into pyx-Ase vector. The library tag  
 sequence located between the Not I site and the polyA  
 tail, is TGAGAGAGCC. This library was created for the  
 University of Iowa Mouse Brain Molecular Anatomy Project  
 (BMAP). 'Gene Discovery in the Developing Mouse Nervous  
 System', supported by National Institutes of Mental Health  
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN  
 Query Match 20.9%; Score 752; DB 6; Length 755;  
 Best Local Similarity 99.7%; Pred. No. 7.4e-178;  
 Matches 752; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 CB245079.1 GI:28366723  
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 ORGANISM  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 736)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pyx-5.  
 Location/Qualifiers  
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VERSION CF182788.1 GI:33314670  
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SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Mus.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Dr. James Ijz, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP).

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location/Qualifiers  
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGGCGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN  
Query Match 19.1%; Score 690.2; DB 6; Length 702;  
Best Local Similarity 99.4%; Pred. No. 2,8e-162;  
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1983 GCGGTTTATCATATGTGTGAGAAAGAACTATCGGCGGCTTCCTTACCAACTGAGAC 2042  
DB 1 GCGGTTTATCATATGTGTGAGAAAGAACTATCGGCGGCTTCCTTACCAACTGAGAC 60  
QY 2043 ATGCAATCAGGTGGGACACATGATATGCAATCTTCAAAACAATGCGCTTTCA 2102  
DB 61 ATGCAATCAGGTGGGACACATGATATGCAATCTTCAAAACAATGCGCTTTCA 120  
QY 2103 CAGACTGAGCGCAAAAGGCTGCTATATGCGGTGTGTCCTTCACTGAGACCAAGG 2162  
DB 121 CAGACTGAGCGCAAAAGGCTGCTATATGCGGTGTGTCCTTCACTGAGACCAAGG 180  
QY 2163 GCTTCAATTAACAGCTACCTGAGAAAGTTGACCAACCCCTGGGCGGCTGTATCCACT 2222  
DB 181 GCTTCAATTAACAGCTACCTGAGAAAGTTGACCAACCCCTGGGCGGCTGTATCCACT 240  
QY 2223 CCACATGAGGACCAACCACTTCTCCAGACGCTGTCATCTTCACTGAGGAGGACCA 2282  
DB 241 CCACATGAGGACCAACCACTTCTCCAGACGCTGTCATCTTCACTGAGGAGGACCA 300  
QY 2283 ATATCTTTCACACCTGAGCTCAGGAGTACGAGAGTGTGAGATCATCCGCAAG 2342  
DB 301 ATATCTTTCACACCTGAGCTCAGGAGTACGAGAGTGTGAGATCATCCGCAAG 360  
QY 2343 CCATATCCGACACCACTCTGCGCTTATCTTTGGAAACGAGAGGAGGAGATG 2402  
DB 361 CCATATCCGACACCACTCTGCGCTTATCTTTGGAAACGAGAGGAGGAGATG 420  
QY 2403 ACCAGACAGGAGTGTGAACCTCCACCAACGATCCATCGACCGTGTATCGGCTTGA 2462  
DB 421 ACCAGACAGGAGTGTGAACCTCCACCAACGATCCATCGACCGTGTATCGGCTTGA 480  
QY 2463 TGATGACTGCTGTGATCTTGTCTGTGACCAAACTATGCGCAATTAATTTGACAG 2522  
DB 481 TGATGACTGCTGTGATCTTGTCTGTGACCAAACTATGCGCAATTAATTTGACAG 540  
QY 2523 CGAATGATATATGCAAAATTTGGGCTGAGGAGTATGAGAGAACTGGGCTTAC 2582  
DB 541 CGAATGATATATGCAAAATTTGGGCTGAGGAGTATGAGAGAACTGGGCTTAC 600  
QY 2583 AGCCCATTCCTATGATGAGACAGAGACAGGAGATGAGGCTTCAAGGCGAGCTGGAT 2642  
DB 601 AGCCCATTCCTATGATGAGACAGAGACAGGAGATGAGGCTTCAAGGCGAGCTGGAT 660  
QY 2643 TCTACATGCTGTGGCATTCCTGTATACCACT 2678  
DB 661 TCTACATGCTGTGGCATTCCTGTATACCACT 696  
RESULT 11 683 bp mRNA linear EST 05-NOV-2003  
CF913876  
LOCUS B0955F07-5 NIA Mouse Unfertilized Egg cDNA library (Long 1) Mus  
DEFINITION musculus cDNA clone NIA:B0955F07 IMAGE:30477570 5', mRNA sequence.  
ACCESSION CF913876



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/db_xref="taxon:10090"
/clonexref="NIA:B0993E08 IMAGE:30481207"
/dev stage="Unfertilized Egg"
/lab host="DH10B"
/clonexlib="NIA Mouse Unfertilized Egg cDNA Library (long
1)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-pGACTGATGTTCTAGATCGAGCGCGCCCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 2.5 kb. The library was
constructed by Yulan Piao."

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## ORIGIN

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Query Match 18.8% Score 677.8; DB 7; Length 681;
Best Local Similarity 99.7%; Pred. No. 3.7e-159; Indels 0; Gaps 0;
Matches 679; Conservative 0; Mismatches 2;
1436 AAGAGACCAAGAGATGATGATTTTCATTTGAGAGAGATGCTGCAAGTGGCAAG 1495
1 AAGAGACCAAGAGATGATGATTTTCATTTGAGAGAGATGCTGCTCAAGTGGCAAG 60
1496 AAGAGGGAAGTCTTGAACATTTCCGATGCTTACGCGACCTTGTCTTAAACAGAGGCTG 1555
61 AAGAGGGAAGTCTTGAACATTTCCGATGCTTACGCGACCTTGTCTTAAACAGAGGCTG 120
1556 GACCTGTACACAGGCTTACACAGAGAGACATTTCTGTATGCGCATGAGCGAGCG 1615
121 GACCTGTACACAGGCTTACACAGAGAGACATTTCTGTATGCGCATGAGCGAGCG 180
1616 AGCGTATGCGCTGTGTCAGATGATGATCAAGATCAGCGGTAGCGCTTCTCAAGACA 1675
181 AGCGTATGCGCTGTGTCAGATGATGATCAAGATCAGCGGTAGCGCTTCTCAAGACA 240
1676 GACGAGAACCACTTCAAGATGTTGCTGTCTTGTGCGCATGCGCTTCACTGTGCTAAC 1735
241 GACGAGAACCACTTCAAGATGTTGCTGTCTTGTGCGCATGCGCTTCACTGTGCTAAC 300
1736 ATGTACCAACAGATCCGCCACTCAGATGATCTTACAGGGTTTACATGAGAGAGCTTCC 1795
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1796 TACCAACAGATCTGCACTCCGAGAGTGGCAAGGCTTCACTGCGCTTCACTTACAGCA 1855
361 TACCAACAGATCTGCACTCCGAGAGTGGCAAGGCTTCACTGCGCTTCACTTACAGCA 420
1856 CGCATCTGCCGGAGCATGAGCTATTTCACCTTTGACATTTGCTTTTGAACAATGTGG 1915
421 CGCATCTGCCGGAGCATGAGCTATTTCACCTTTGACATTTGCTTTTGAACAATGTGG 480
1916 CTTGGGATCTTTTGTCTACATGATTCATCGGCTTGTGAGACATCTCTTTTGAACCTTGA 1975
481 CTTGGGATCTTTTGTCTACATGATTCATCGGCTTGTGAGACATCTCTTTTGAACCTTGA 540

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QY 1976 AAATGTGCGCGTTTATCATGATCTGTGAAGAAAGATATGCGCGGCTTCTTACCACAC 2035
DB 541 AAATGTGCGCGTTTATCATGATCTGTGAAGAAAGATATGCGCGGCTTCTTACCACAC 600
QY 2036 TGAAGACATGACATGACCGGTGGCACATGCTGATGCTTATCTTCAAAACAAATGGC 2095
DB 601 TGAAGACATGACATGACCGGTGGCACATGCTGATGCTTATCTTCAAAACAAATGGC 660
QY 2096 CTCTTACAGACCTTGAAGCGC 2116
DB 661 CTCTTACAGACCTTGAAGCGC 681

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RESULT 13
LOCUS BM230520/c 671 bp mRNA linear EST 07-JUN-2003
DEFINITION Mus musculus cDNA clone NIA:K0296G04 IMAGE:30053931 3', mRNA sequence.
ACCESSION BM230520
VERSION BM230520.2 GI:31487884
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 671)
Piao, Y., Ko, N.-T., Lim, M. K. and Ko, M. S. H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
11544199
JOURNAL PUBMED
COMMENT On Dec 14, 2001 this sequence version replaced gi:17793762.
CONTACT Dawood B. Dudekula
LABORATORY OF GENETICS
NATIONAL INSTITUTE ON AGING/NATIONAL INSTITUTES OF HEALTH
333 CASSELL DRIVE, SUITE 4000, BALTIMORE, MD 21224-6820, USA
EMAIL: cdna@igsun.grc.nia.nih.gov
PLATE: K0296 ROW: G COLUMN: 04
SEQ PRIMER: -21M13 Forward
HIGH QUALITY SEQUENCE STOP: 671
POLY-A=Yes.

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## FEATURES

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location/Qualifiers
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/issue_type="Unfertilized Egg"
/lab host="DH10B"
/clonexlib="NIA Mouse Unfertilized Egg cDNA Library
(long)"
/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
primer (Invitrogen):
5'-pGACTGATGTTCTAGATCGAGCGCGCCCTTTTCTTTT-3',
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes

```

and cloned into Sali/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.5 Kb. The library was constructed  
by Yulan Piao (NIA)."

## ORIGIN

Query Match 18.6%; Score 671; DB 3; Length 671;  
Best Local Similarity 100.0%; Pred. No. 1.9e-157; Mismatches 0; Indels 0; Gaps 0;  
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2878 GCAACCGACTCAACCTGCTTCTGTGATCTCTCTTTTGTGTTTCAAGGGGTGAAAACCC 2937  
671 GCAACCGACTCAACCTGCTTCTGTGATCTCTCTTTTGTGTTTCAAGGGGTGAAAACCC 612

2938 CCTGTCAAGAGTACCGTGCATATCATGTGAGACAGACGACTCCCTGCTCCGCACAC 2997  
611 CCTGTCAAGAGTACCGTGCATATCATGTGAGACAGACGACTCCCTGCTCCGCACAC 552

2998 CACCTCGACAGTGAAGCAACCGGCTGCGGTGTGAGAGTGGGGCTACTCGGTGGCT 3057  
551 CACCTCGACAGTGAAGCAACCGGCTGCGGTGTGAGAGTGGGGCTACTCGGTGGCT 492

3058 CCACCTGACCTCCGATGCTATTTGCTCCCAAGGACGACACTGCTGTGAGAGGGAGCA 3117  
491 CCACCTGACCTCCGATGCTATTTGCTCCCAAGGACGACACTGCTGTGAGAGGGAGCA 432

3118 GAGACCAAGAGAGGTTCTTCCCTGCATCTCTCCATGAGGGTGTGGCCATTTCCCTGCT 3177  
431 GAGACCAAGAGAGGTTCTTCCCTGCATCTCTCCATGAGGGTGTGGCCATTTCCCTGCT 372

3178 TCTGTGCATGCTGCTGCTGTGGTGCATTTGTTAGGAAGGGACACAGGCCCTTGTTGT 3237  
371 TCTGTGCATGCTGCTGCTGTGGTGCATTTGTTAGGAAGGGACACAGGCCCTTGTTGT 312

3238 GAAAGTTACATGTGACCTTCTTATAGTTAACTGAGTTTGTGGCTGGGACACATGTAAT 3297  
311 GAAAGTTACATGTGACCTTCTTATAGTTAACTGAGTTTGTGGCTGGGACACATGTAAT 252

3298 GAAAGTCAACAGTCCACAGGTGACAGGAATCCAACTGTTGATTAACAGTGCACCTACAG 3357  
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3358 GTATGCTCTTTCAGTCTATCTGGGGGACATAGTGAAGTGTGCTCCTACCTCAGAGGAAGC 3417  
191 GTATGCTCTTTCAGTCTATCTGGGGGACATAGTGAAGTGTGCTCCTACCTCAGAGGAAGC 132

3418 ATACCTCTGCTCCCTCACTCAGAGGACACAGGGTACATCCAGGACATCGGGGAATGAACT 3477  
131 ATACCTCTGCTCCCTCACTCAGAGGACACAGGGTACATCCAGGACATCGGGGAATGAACT 72

3478 CTCACTTCAAAACATGTCAAAAGATTAAACACCTCCCTCCCTCACTGTAAGCTTGC 3537  
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RESULT 14  
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LOCUS DEFINITION UI-M-G20-cjn-b-10-0-UI.r1 NIH\_BMAP\_G20 Mus musculus cDNA clone  
IMAGE:30604737 5', mRNA sequence.  
CF725825  
ACCESSION CF725825  
VERSION CF725825.1 GI:37599993  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 680)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: PYX-5.

## FEATURES

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Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to RNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into PYX-Aac vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TTAATGAAGT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

## ORIGIN

Query Match 18.6%; Score 670.2; DB 6; Length 680;  
Best Local Similarity 98.8%; Pred. No. 3e-157; Mismatches 8; Indels 0; Gaps 0;  
Matches 672; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

677 AGCAGGTACAGATACGAATATGCAAGGAGTGTGTGACAGCTGACATTAAGAG 736  
1 AGCAGGTACAGATACGAATATGCAAGGAGTGTGTGACAGCTGACATTAAGAG 60

737 CAGCCCTGAGACAGGGGGGGAACAACCTGCTCTCTATAGACTACAGACGATCATC 796  
61 CAGCCCTGAGACAGGGGGGGAACAACCTGCTCTCTATAGACTACAGACGATCATC 120

797 AGGATAGCCAAAAGCCGAGGATTTGACATGTAATCTCTTGAGAGTGCATAATATAGC 856  
121 AGGATAGCCAAAAGCCGAGGATTTGACATGTAATCTCTTGAGAGTGCATAATATAGC 180

857 CTGTGTGTTCATACCAACCCGGATGAAGAGCCAAACCCGGCTCATCCCTGACGGG 916  
181 CTGTGTGTTCATACCAACCCGGATGAAGAGCCAAACCCGGCTCATCCCTGACGGG 240

917 CCCATCACCCAGGGTACACCATCTCTGCTTACGTGGCCAAAGTCTAGAGAAAGCTTTGTTG 976  
241 CCCATCACCCAGGGTACACCATCTCTGCTTACGTGGCCAAAGTCTAGAGAAAGCTTTGTTG 300

977 GTAAGATATCTTTGGGGATGAGGATTTCTCTGAGGTACTGCGCTGGAATCAGAAAC 1036  
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1037 CGCATCCAGTCTGTCTTTGCTTGGCCCATTTGTCATGTCATGAGACTTGAATTTGGCATC 1096



Db 361 GCATCCAGCTCTTCTTCTTCTTCCCAATGTCTACTGCCATTGGAGACTTGTGGCATC 420  
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Qy 1337 GCCGACCGCTGCGCGCTCTT 1356  
Db 661 GCCGACCGCTGCGCGCTCTT 680

RESULT 15  
LOCUS CX241102 662 bp mRNA linear EST 29-DEC-2004  
DEFINITION NM\_03974 Mus Musculus Lateral Ventricle Wall C57BL/6 adult Mus  
ACCESSION CX241102  
VERSION CX241102.1 GI:56896394  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 662)  
AUTHORS Williams, C., Wirtz, W., Wikstrom, L., Lundberg, J. and Friese, J.  
TITLE Expressed sequence tags of cDNA clones from Mus Musculus Lateral  
Ventricle Wall  
JOURNAL Unpublished (2005)  
COMMENT Contact: Erlendsson, R.  
Target Identification  
NeuroNova AB  
Piskarcorpavagen 15A-D, S-11433 Stockholm, Sweden  
Tel: +46 8 786 0915  
Fax: +46 8 786 0911  
Email: rikard.erlandsson@neuronova.com  
Seq primer: M13FWD.

FEATURES  
source location/Qualifiers

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adult"  
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Site 2: EcoRV; An oligo(dT) primed library was constructed  
in pCMVSPORT6 from RNA isolated from lateral ventricle  
wall tissue of adult male and female mice."

ORIGIN

Query Match 17.9%; Score 646.4; DB 8; Length 662;  
Best Local Similarity 99.7%; Pred. No. 3e-151; 1; Indels 1; Gaps 1;  
Matches 658; Conservative 0; Mismatches 1; Gaps 1;  
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Db 1 GGAAAGCCAAACCCGGCTATCCCTGAGGCGCCATCACCAGGATACCAACATCTCTGC 60  
Qy 946 CTAAGTGGCCAAAGTCTAGAAAGACGTTGTGTAGAGATATCTTGGGAGATGACGATTT 1005  
Db 61 CTAAGTGGCCAAAGTCTAGAAAGACGTTGTGTAGAGATATCTTGGGAGATGACGATTT 120  
Qy 1006 TCTTCAGAGTACTGGCTCGGAATCAGGAACCCGCAATCAGTCTGTTCTTGGTGGCCAT 1065  
Db 121 TCTTCAGAGTACTGGCTCGGAATCAGGAACCCGCAATCAGTCTGTTCTTGGTGGCCAT 180  
Qy 1066 TGTCACTGCCAATTTGAGAGCTTGAATTTGATGATCTTGAATCTGATACAGGCACTGGGGCAAGA 1125  
Db 181 TGTCACTGCCAATTTGAGAGCTTGAATTTGATGATCTTGAATCTGATACAGGCACTGGGGCAAGA 240  
Qy 1126 GGCCTTCTGCTTCAGCCATCAGAGGTTTGAACAGCCATCTTGTGGGCTTCCGTAGC 1185  
Db 241 GGCCTTCTGCTTCAGCCATCAGAGGTTTGAACAGCCATCTTGTGGGCTTCCGTAGC 300  
Qy 1186 AATACACAGGTGCAAGTGTGTAGAGCTTCGCCAAGACAGCCGAATGAATGACTTCT 1245  
Db 301 AATACACAGGTGCAAGTGTGTAGAGCTTCGCCAAGACAGCCGAATGAATGACTTCT 360  
Qy 1246 ACTGAGGATCAAGACATCTTGTATATACATAGTTCATAGACTCTTACTTGAACA 1305  
Db 361 ACTGAGGATCAAGACATCTTGTATATACATAGTTCATAGACTCTTACTTGAACA 420  
Qy 1306 CATCATGATATATGCAAAAAATCTAGTGAACGCGGCTGCGCTTCTTCAAGTGA 1365  
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Qy 1366 CCACAAAGCAAGAGCTGTACTCGAAGCTGTTGACATTTGGGAGAGAGAGAGGGA 1425  
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Qy 1426 GCCCATCTTCAAGAGACCAAGAGATGATTTTCAATTGAGAAAGGATGTGTGTC 1485  
Db 541 GCCCATCTTCAAGAGACCAAGAGATGATTTTCAATTGAGAAAGGATGTGTGTC 600  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 03:08:59 ; Search time 607 Seconds  
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10559.946 Million cell updates/sec

Title: US-10-618-252-14

Perfect score: 3606  
Sequence: 1 acgcgcgcgcctccatctg.....aatttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/H COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq: \*  
7: /cgn2\_6/prodata/1/ina/PE COMB.seq: \*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq: \*  
9: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1871.8	51.9	4389	2 US-08-951-648-3	Sequence 3, App1
2	1871.8	51.9	4389	3 US-09-174-437-3	Sequence 3, App1
3	1871.8	51.9	4389	3 US-09-686-055A-3	Sequence 3, App1
4	1871.4	49.6	3195	2 US-08-951-648-5	Sequence 5, App1
5	1871.4	49.6	3195	3 US-09-174-437-5	Sequence 5, App1
6	1871.4	49.6	3195	3 US-09-686-055A-5	Sequence 5, App1
7	1871.4	49.6	4381	3 US-09-420-190-2	Sequence 2, App1
8	1785	49.5	2298	2 US-08-951-648-1	Sequence 1, App1
9	1785	49.5	2298	3 US-09-174-437-1	Sequence 1, App1
10	1785	49.5	2298	3 US-09-686-055A-1	Sequence 1, App1
11	469.2	13.0	477	2 US-08-951-648-38	Sequence 38, App1
12	469.2	13.0	477	3 US-09-174-437-38	Sequence 38, App1
13	469.2	13.0	477	3 US-09-686-055A-38	Sequence 38, App1
14	333.8	9.3	404	2 US-08-951-648-33	Sequence 33, App1
15	333.8	9.3	404	3 US-09-174-437-33	Sequence 33, App1
16	333.8	9.3	404	3 US-09-686-055A-33	Sequence 33, App1
17	272.6	7.6	458	2 US-08-951-648-7	Sequence 7, App1
18	272.6	7.6	458	3 US-09-174-437-7	Sequence 7, App1
19	272.6	7.6	458	3 US-09-686-055A-7	Sequence 7, App1
20	209.6	5.8	3044	2 US-07-872-644-4	Sequence 44, App1
21	209.6	5.8	3044	2 US-08-297-494-44	Sequence 44, App1
22	209.6	5.8	3044	2 US-08-297-510-44	Sequence 44, App1
23	209.6	5.8	3044	2 US-08-479-532-44	Sequence 44, App1
24	209.6	5.8	3044	2 US-08-455-526-44	Sequence 44, App1

25	209.6	5.8	3044	2 US-08-455-525-44	Sequence 44, App1
26	209.6	5.8	3044	3 US-09-139-491-44	Sequence 44, App1
27	209.6	5.8	3044	3 US-09-883-825-44	Sequence 44, App1
28	209.6	5.8	3044	6 PCT-US92-03222-44	Sequence 44, App1
29	209.6	5.8	4171	3 US-09-754-250-1	Sequence 1, App1
30	209.6	5.8	4171	3 US-10-094-989-1	Sequence 1, App1
31	209.6	5.8	4240	3 US-09-708-392-6	Sequence 373, App1
32	209.6	5.8	4240	3 US-09-949-016-373	Sequence 373, App1
33	201.6	5.6	1784	3 US-09-226-741-2	Sequence 2, App1
34	201.6	5.6	1784	3 US-09-595-514-2	Sequence 2, App1
35	192.8	5.3	3789	2 US-07-872-644-42	Sequence 42, App1
36	192.8	5.3	3789	2 US-08-297-494-42	Sequence 42, App1
37	192.8	5.3	3789	2 US-08-297-510-42	Sequence 42, App1
38	192.8	5.3	3789	2 US-08-479-532-42	Sequence 42, App1
39	192.8	5.3	3789	2 US-08-455-525-42	Sequence 42, App1
40	192.8	5.3	3789	2 US-08-455-525-42	Sequence 42, App1
41	192.8	5.3	3789	3 US-09-139-491-42	Sequence 42, App1
42	192.8	5.3	3789	3 US-09-883-825-42	Sequence 42, App1
43	192.8	5.3	3789	6 PCT-US92-03222-42	Sequence 42, App1
44	192.8	5.3	4131	2 US-07-872-644-38	Sequence 38, App1
45	192.8	5.3	4131	2 US-08-297-494-38	Sequence 38, App1

#### ALIGNMENTS

RESULT 1  
US-08-951-648-3  
Sequence 3, Application US/08951648  
Patent No. 5932465  
GENERAL INFORMATION:  
APPLICANT: Loughney, Kate  
TITLE OF INVENTION: Phosphodiesterase 8  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker, Sears Tower Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/951,648  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27666/34038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4389 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..2411  
US-08-951-648-3  
Query Match 51.9%; Score 1871.8; DB 2; Length 4389;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

415 CTTCCCCCTGCGCAGCGTTTGCGCGCTTGCGGCTCCGACATGAGAAAGATGAGACCCCTC 474  
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Db 302 TGAACCTGAACAGCTATATGAG 361  
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542 CAAGCTCTAGAGAGAGAGT 601  
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1255 ATCAAAGCATATCTTGAATATATAGTGTGCACTGCTCTACTGTAACATCATAT 1314  
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1142 AGACTGTATCAACAGAGCTATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201  
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1675 AG 1734  
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1795 CTACCAAGAGATCTGCACTCCGAG 1854  
Db 1382 CTACCATGAGATTTGTATCTTGAAG 1441  
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2155 CCAAG 2214  
1742 CCAAG 1801  
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1802 CTCGACTTCAACAG 1861  
2275 AGGAGCAATATCTTTTCCAG 2334  
1862 AGGAGCAATATCTTTTCCAG 1921  
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2395 GAGAGATGAG 2454  
1982 AGAGATGAG 2041  
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2042 TGGTTTGTATGAG 2101  
2515 ATTGAG 2574  
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2575 GGGGATACAGGCAATCTCTATGATGAG 2634

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RESULT 2  
US-09-174-437-3  
/ Sequence 3, Application US/09174437A  
/ Patent No. 6133007  
/ GENERAL INFORMATION:  
/ APPLICANT: Loughney, Kate  
/ TITLE OF INVENTION: Phosphodiesterase 8A  
/ FILE REFERENCE: 27866/35047  
/ CURRENT APPLICATION NUMBER: US/09/174,437A  
/ EARLIER APPLICATION NUMBER: 08/951,648  
/ EARLIER FILING DATE: 1998-10-16  
/ NUMBER OF SEQ ID NOS: 48  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 3  
/ LENGTH: 4389  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (3)..(2411)  
US-09-174-437-3

Query Match 51.9%; Score 1871.8; DB 3; Length 4389;  
Best Local Similarity 86.5%; Pred. No. 0;  
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

QY 415 CTTCCCTCTTGCCACCGTTTGCGCTGCTCCCTTGCTCGACATGAGAGATGACCTTC 474  
Db 2 CTTCCCTCTTGCGCGCGCGCGCTGCTCTTGCTCGACATGAGATGACCTTC 61  
QY 475 TAAAGATGGAATGTTGCTTCCGAAAGCTGACCGAGTGTTCCTGAGCCCACTTGAAG 534  
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QY 595 AAGCTGTAAGTGAAGACTGTGAGAAAGTGGCTGAAGAGAGAAACCAACAAAGCAAGA 654  
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QY 835 CTTTGAAGATGCAATATAGCTGTGTGTCTATACCAACCCGGAGTGAAGAGGCCA 894  
Db 422 CTTTGAAGATGCAATATAGCTGTGTGTCTATACCAACCCGGAGTGAAGAGGCCA 481

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Db 482 ACCCGGCTCATCCCTGAGAGGCCCATGACCCAGGATACCAACATCTGAGCTAGTGGC 541  
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Db 602 TACTGAGCTGGAATCAGAGACTCGATCAGTCTGTCTTTGCTTGAACAAATGTCACTGC 661  
QY 1075 CATTTGAGACTGATTTGGCATCTCTTGAACCTGACAGCACTGGGGCAAGAGCCCTCG 1134  
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Db 1322 TATGTATCATGAATTCGCACTCAGAGTGCATTTACGGGATAGAGTGAAGAGCTGC 1381  
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QY 1915 GCTGGGATCTTGTCTACATGATTCATGCTTGTGAGACATCTGCTTTTGAACCTTGA 1974  
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QY 1975 AAAATTGTCGCTTTATCATGCTGTGTGAAGAAGAACTATCGGCGGGTTCTTACACAA 2034
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DB 1742 CCACAGGGGCTTCAATACAGTACCTGAGAAAGTTGACACACCCCTGGCGGGCTTCTTA 1801
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DB 1862 AGGGCAATATCTTCTCCACCTTGAAGCTCCAGCGATACAGAGGTGTGTGAGATCAT 1921
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DB 1922 CCGCAAGGCATCATGCGACCGACCTGCTGCTTATCTTGGGAAACAGGAACATTTGA 1981
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## RESULT 3

US-09-686-055A-3

Sequence 3, Application US/09686055A

Patent No. 6566087

GENERAL INFORMATION:

APPLICANT: Loughney, Kate

TITLE OF INVENTION: Phosphodiesterase 8A

FILE REFERENCE: 27866/35047

CURRENT APPLICATION NUMBER: US/09/686,055A

CURRENT FILING DATE: 2000-10-11

PRIOR APPLICATION NUMBER: 08/951,648

PRIOR FILING DATE: 1997-10-16

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 4389

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3) .. (2411)
US-09-686-055A-3

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Query Match      51.9%; Score 1871.8; DB 3; Length 4389;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

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QY 415 CTTCCCTTCGCAACGCTTTGCGCTGCTCCGCTCCGACATGGAATGACCTTC 474
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QY 475 TAAATATGCGAGCTGCTTCCGAAAGCTGACCGAGTGTCTTCCAGCCCCAGTTTGACGA 534
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DB 482 ACCCGGCTCATCCCTGAGGAGGAGGATCAACCAAGGATTCACATCTGCTACGTGC 541
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Db 1202 CAGCGTGAATGGCGTGTGAGATGATGAAACAAATCAGCGGATCGCTTCTCAAGAC 1261  
Qy 1675 AAGAGGAAACCACTTGAAGATGTTTGTCTGTGCGACCTGCGCTTGACGTGTAA 1734  
Db 1262 AAGTGAACCACTTGAAGATGTTTGTCTGTGCGACCTGCGCTTGACGTGTAA 1321  
Qy 1735 CATGTACACAGAGTCCGCACTCAGAAATGATCTACAGGGTTTACCAAGAGAGCTTTC 1794  
Db 1322 TATGTATCATGAATTCGCACTCAGAGTCAATTTACGGGTAAACATGGAAGAGCTGTC 1381  
Qy 1795 CTACCAAGAGATCTGACCTCGAGAGATGGCAAGGCTCTGATCGCTTCAACTACAC 1854  
Db 1382 CTACCAAGAGATCTGATCTTCAAGAAAGTGGCAAGGCTCTGATCTCAATCTCCCT 1441  
Qy 1855 AGGCACTGCGCGGAGATGAGATATTCACCTTTGACATTTGTCTTGAGAAACATGTC 1914  
Db 1442 GCGTCTGTGAAAGAAATGAATTAATTCACCTTTGACATTTGTCTTGAGAAACATGTC 1501  
Qy 1915 GCGTGGGATCTTTGTCTACATGATCATCGGTCTTTGGAGCATCTGTTTGAACCTGA 1974  
Db 1502 GCGTGGGATCTTTGTCTACATGATCATCGGTCTTTGGAGCATCTGTTTGAACCTGA 1561  
Qy 1975 AAAATGTGCGGTTTATCATGATCTGTGAGAAAGAACTATGCGCGGGTCTTTACCA 2034  
Db 1562 AAAATGTGCGGTTTATCATGATCTGTGAGAAAGAACTATGCGCGGGTCTTTATCA 1621  
Qy 2035 CTGGAAGCATGAGTCAAGGTGCACTGAGATGATGCTTCAAAACCAATAGG 2094  
Db 1622 CTGGAAGCATGAGTCAAGGTGCACTGAGATGATGCTTCAAAACCAATAGG 1681  
Qy 2095 CCTCTTCAAGACCTGAGGCGAAAGGCTGTAATGCGTGTCTGTGCAATGACCTGA 2154  
Db 1682 GCTTTTCAAGACCTGAGGCGAAAGGCTGTAATGCGTGTCTGTGCAATGACCTGA 1741  
Qy 2155 CCAAGAGGCGCTTCAAGTAAACGTAACCTGAGAAAGTTGACACCCCTGCGCGCTGA 2214  
Db 1742 CCAAGAGGCGCTTCAAGTAAACGTAACCTGAGAAAGTTGACACCCCTGCGCGCTGA 1801  
Qy 2215 CTGCACTTCAAGTGAAGCAACCACTTCTCCAGAGGTGTCCATCTTTCAAGCTGA 2274  
Db 1802 CTGCACTTCAAGTGAAGCAACCACTTCTCCAGAGGTGTCCATCTTTCAAGCTGA 1861  
Qy 2275 AGGAGCAATATCTTCTCAAGCTGAGCTGAGAGTACAGAGAGGTGCTGAGATCAT 2334  
Db 1862 AGGAGCAATATCTTCTCAAGCTGAGCTGAGAGTACAGAGAGGTGCTGAGATCAT 1921  
Qy 2335 CCGCAAGGCAATATCTTCTCAAGCTGAGCTGAGAGTACAGAGAGGTGCTGAGATCAT 2394  
Db 1922 CCGCAAGGCAATATCTTCTCAAGCTGAGCTGAGAGTACAGAGAGGTGCTGAGATCAT 1981  
Qy 2395 GGAATGTACAGAGAGGTGCTGAGCTTCCACCAACCAATGCTTCAAGAGAGGTGCTCAT 2454  
Db 1982 AGAATGTACAGAGAGGTGCTGAGCTTCCACCAACCAATGCTTCAAGAGAGGTGCTCAT 2041

Qy 2455 CCGCTTGAATGATGATCTGCTGTGATCTTTGCTGTGACCAAACTATGCGCCAGTTACAA 2514  
Db 2042 TGGTGTGATGATGATGCTGCTGTGATCTTTGCTGTGACCAAACTATGCGCCAGTTACAA 2101  
Qy 2515 ATTGAAGGCAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATGAAGAGCT 2574  
Db 2102 ATTGAAGGCAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATGAAGAGAT 2161  
Qy 2575 GGGCATACAGCCCATCTCTATGATGAGACAGAGCAAGGAGTGAAGTCTTCAAGGCA 2634  
Db 2162 GGGCATACAGCCCATCTCTATGATGAGACAGAGCAAGGAGTGAAGTCTTCAAGGCA 2221  
Qy 2635 GCTGGAATTTCAATATGCTGTGCGCATTCCTGCTATACACCTTGAAGCAGATCTCC 2694  
Db 2222 GCTGGAATTTCAATATGCTGTGCGCATTCCTGCTATACACCTTGAAGCAGATCTCC 2281  
Qy 2695 ACCCAAGAGCTCTGCTGAAGGCTGAGAGGATTAACCTCAATCAGTGGAGAGATAT 2754  
Db 2282 TCCCAAGAGCTCTGCTGAAGGCTGAGAGGATTAACCTCAATCAGTGGAGAGATAT 2341  
Qy 2755 TCGCGGAGAGAGACAGCAATGTGATTTCAAGCCCAAGCCCGGCGC 2801  
Db 2342 TCGAGGAGAGAGACAGCAATGTGATTTCAATCCCATCCGCGCTC 2388

RESULT 4  
US-08-951-648-5  
Sequence 5, Application us/08951648  
Patent No. 5932465  
GENERAL INFORMATION:  
APPLICANT: Loughney, Kate  
TITLE OF INVENTION: Phosphodiesterase 8  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker, Sears Tower Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/951,648  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/34038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3195 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 67..2403  
US-08-951-648-5  
Query Match 49.6%; Score 1787.4; DB 2; Length 3195;  
Best Local Similarity 86.6%; Pred. No. 0;  
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;



Db 2264 AGATCTCCCTCCACGAGCCTCTTCTGAAGCATGACGAGTAATCTCACTCACTGGG 2323  
QY 2745 AGAAGTAATTCGCGGGAAGAGACAGCAATGTGATTTTCAGGCCCGCGGC 2801  
Db 2324 AGAAGTAATTCGAGGGGAGAGACAGCACTGATTTTCATCCCATCTGCGCTC 2380

RESULT 5  
US-09-174-437-5  
; Sequence 5, Application US/09174437A  
; Patent No. 6133007  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/174,437A  
; CURRENT FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 08/951,648  
; EARLIER FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3195  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)..(2403)  
US-09-174-437-5

Query Match 49.6%; Score 1787.4; DB 3; Length 3195;  
Best Local Similarity 86.6%; Pred. No. 0;  
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

QY 525 GTTTGACGATGAAGCGTGAAGCCATCTCTCCATCCCGGTAATTGATGAAT 584  
Db 104 GTTTGACAGTGAAGAAAGTGAAGCAATCTTCTTCACCCGATTAATGATGAAT 163  
QY 585 TTGTTCTGAAAGTGTAGTGACAGAGCTGTGAAAAAGTGGCTGAAGAGAAAAACA 644  
Db 164 TTGTATCTGAAGTGTAGTGACAGAGCACTAGAGAAATGGCTGAAGAGAAACA 223  
QY 645 AAGCAAAAGATGAACCATCTCCAGAGAGTCAAGAGTACAGATACGAATATGCA 704  
Db 224 AATCAGAAAGATGAATCGGCTCTTAAGAGAGTCAAGAGTACCAAGATACCA 283  
QY 705 GAGTCTGTACAGAGTGAACAGCTACATAGAGAGCGCTGACAGGGGGGGAACA 764  
Db 284 GAGTGTATATGAACATAAGAGCTATATAGAACAGCGTTGACACAGAGAGACA 343  
QY 765 ACCTGCTCCCTATAGAGCTCAGAGCATCATCAGATAGCCAAAGCCGAGATTG 824  
Db 344 AGCTACTCTCTATAGACTAGAGCATCATTAATAATAGCCAAAGCCGAGATTG 403  
QY 825 CACTGTACTTCTTGAAGAGTGAATTAAGCCGTGTGTGTTTCAATCAACCCGGATG 884  
Db 404 CACTGTATTTCTTGAAGAGTGAATTAAGCCGTGTATATTCAACCCGAGATTG 463  
QY 885 AGAAGGCCAACCCCGGCTCATCTCTGAGGGCCATCAACAGGGATCAACCATCT 944  
Db 464 AGAAGGAAAAACCCCGCTCATCTCTGAGGGCCATCAACAGGGACACACGTC 523  
QY 945 CCTACGAGCCCAAGTCAAGAGAGCTTGTGTGAGAGATATCTCTTGGGAGAGCAT 1004  
Db 524 CTTATGTGGCAAGTCCAGAGAAACACTGCTAGTGAAGACATCTTGGAGATGA 583  
QY 1005 TTCTCGAGGTACTGCGCTGGAATCAGAAACCGCATCAAGTCTGTTCTTGGCCA 1064  
Db 584 TTCGAAGAGGTACTGAGCTGGAATCAGGAGCTGATTCAGTCTGTTCTTGGCTTA 643  
QY 1065 TTGTCACTGCAATTTGAGACTGATTTGATCTCTTGAACGTGTAACAGGCACT 1124  
Db 644 TTGTCACTGCAATTTGAGACTGATTTGATCTCTGAGCTGATCGGCACTGGGG 703

QY 1125 AGGCTTTGCTGCTCAGCCATCAGAGAGGTTGCAAGCCATCTTCTGAGGCTTCG 1184  
Db 704 AAGCCTTCTGCTTATGTAACAAGAGGTTGCAACAGCAATCTTCTGAGGCTTC 763  
QY 1185 CAATACACAGGTGAGGTGTGTAGAGGTCTGCCAAACAGCCGACTGAATGACTTC 1244  
Db 764 CAATACATCAGGTGAGGTATGCAAGGCTTGGCAACAGCAAGATTAATGACTTC 823  
QY 1245 TACTGAGGTATCAAAAGATATCTTGTATACATATGTTGCCATTAACCTCTTA 1304  
Db 824 TACTGAGGTATCAAAACATATTTGATTAATATGTTGCAATATCTTCACTTGA 883  
QY 1305 ACATCATATATATATCAAAAAATCTAGTAAGCCGACCGCGCGCTTCCAGGTG 1364  
Db 884 ACATATATATATATCAAAAACTGTGTAATGCGATGTTGTGCACTTTTCAAGT 943  
QY 1365 ACCCAAGAACAGAGAGCTGTACTGGAACCTGTTGACATTTGGAGAGAGAGG 1424  
Db 944 ACCATAGAACAGAGAGTATATATGAGCTTTTGAATTTGAGAGGAAAGAGAA 1003  
QY 1425 AGCCATCTTCAAGAACCAAGAGATCAATTTTCCATTGAAAGAGGATTTGCT 1484  
Db 1004 AACCTGTCTTCAAGAACCAAGAGATTAATTTTCAATTAAGAAAGAAATTTG 1063  
QY 1485 AAGTGCAGAAAGACAGCGCAAGTCTTGAACATTCGCGATGCTTACGCGCTTA 1544  
Db 1064 AAGTGCAGAAAGACAGCGCAAGTCTGAAATTTCCAGATCTTATGACAGCC 1123  
QY 1545 ACAGGAGGTGACCTGTACAGAGCTTACACAGAGAACATTTGTATATCCATAG 1604  
Db 1124 ACAGAGAGTATATCTTGTACAGAGTACACACCGGAAACATCTGTGATGCG 1183  
QY 1605 TGAAGCGAGACCGTGTATGCGTGTGCAATGTGTAACAAAGTCAAGCGT 1664  
Db 1184 TGAAGCGAGACCGTGTATGCGTGTGCAATGTGTAACAAAGTCAAGCGT 1243  
QY 1665 TCTCCAGACACAGAGAACATTTGATGCTCTTCTGCGCACTGCGCTTCG 1724  
Db 1244 TCTCTAAACAGATGAACCACTTCAAAATGTTTGCCTTCTTGTGCTTAA 1303  
QY 1725 ACTGTCTAACTGTACACAGATCCGCACTCAGATGATCTTACAGGGTTAC 1784  
Db 1304 ACTGTCTAACTGTATCATATGATTTGCGCACTCAGATGATCTTACAGGG 1363  
QY 1785 AGAAGCTTCTTACCAACAGATCTGCACTCCGAGAGTGGCAAGGCTCAT 1844  
Db 1364 AAGAGCTCTTACCAATGATTTGATTCAGAGAGTGGCAAGGCTCATGCA 1423  
QY 1845 ACCTTACAGACGATCTGCGCGGACATGAGCTATTCACTTTGACATTTG 1904  
Db 1424 CCCTTCCCGTGTCTCTCAAGAAATTAATTTTCACTTTGACATTTGCT 1483  
QY 1905 AGAAGATGTGGCTGTGGATCTTGTCTACATGATCCATGAGTCTTGGGCA 1964  
Db 1484 AAGAGATGTGGCTGTGAATTTTGTCTACATGATTTGATGAGTCTTGGGCA 1543  
QY 1965 TTGAATTTGAATTTGTGCGGTTTATCATGTCTGTGAAGAACTATCGCG 2024  
Db 1544 TTGAATTTGAATTTGTGCGGTTTATCATGTCTGTGAAGAACTATCGCG 1603  
QY 2025 CTTTACCAACATGGAAGCATGATGCAAGTGGCAACATGATATGCAATCTT 2084  
Db 1604 CTTTATCAACATGGAAGCATGAGCTGATGCAACATGATATGCAATCTTCA 1663  
QY 2085 ACAACATGAGCTCTTCAACAGCTTCAAGGCGCTGATTAATGCTGTCTG 2144  
Db 1664 ACATATCACAGCTTTTCAACAGCTTGAAGGCAAGAGCTGATTTGCGTGT 1723  
QY 2145 ATGACCTGACCAACAGGCGCTTCAATACATGATCTTCAAGAGTTCACAC 2204  
Db 1724 ATGACCTGACCAACAGGCGCTTCAATACATGATCTTCAAGAGTTCACAC 1783

QY	2205	CGGCGCTGTATCTCCACCTCTCCACCAATGAGAGCAACACACTTCTCTCCAGACGGTGTCCATCC	2266
Db	1784	CGCGTCTCTACTCTCCACTTCCACCAATGAGAGCAACACTTCTCTCCAGCTGTGTCCATCC	1843
QY	2265	TTCAAGCTGGAAGGGCAACATATCTCTCCACCTGAGCTCCAGCGAGTACAGACAGGTGC	2324
Db	1844	TCCAGTTGGAAAGGGCAACATATCTCTCTCCACTGTAGCTCCAGTGAATATAGACAGGTGC	1903
QY	2325	TGGAGATCATCTCGCAAGCCATCATCTGCACCGACCTCGCCCTATATCTTTGGGAAACAGGA	2384
Db	1904	TTGGAGATCATCTCGCAAGCCATCATCTGCACAGACCTTGCTTTATATCTTTGGAAACAGGA	1963
QY	2385	AGCAGTTGGAAGAGATGTACCAAGACAGGGTGGCTGTAACCTCCACAACAGTCCCATCGAG	2444
Db	1964	AGCAGTTGGAAGAGATGTACCAAGACCGGATCATCTAAACCTTAATATCAATCACTTAAG	2023
QY	2445	ACCCTGTATCGGCTTGATGTATGATGTGCTGTGATCTTGTGCTGTGTGACCAATCTATGGC	2504
Db	2024	ACCCTGTATTTGGTTTGTATGTATGATGTGCTGCTGTGACCTTTGTCTGTGACAAACTGTGGC	2083
QY	2505	CAGTTTCAAAATTTGACAGCGAATGATATATATATGCAAAATTCCTGGGCTGAGGGGTGATGGA	2564
Db	2084	CCGTTCACAAATTTGACCGGCAATGATATATATATGCAAAATTCCTGGGCTGAGGGGTGATGAA	2143
QY	2565	TGAAGAGCTGGGCTATACGCCCATTTCTATATGTAGACAGACACAGGGAATGAAGTCC	2624
Db	2144	TGAAGAAATTTGGGAATATACGCCCTATTTCTATATGTAGACAGACACAGGAGATGAAGTCC	2203
QY	2625	CTCAAGGGCAGACTCGAATTTCTACATGTGTGGCCATTCCTCGCTATATCAACCTTGACGC	2684
Db	2204	CCCAAGGCGAGCTTGGGTTTCTACATGTGCGGTGGCCATTCCTCGCTATATCAACCTTGACCC	2263
QY	2685	AGATCTTCCACCCACAGAGCCTCTGCTGAAGGCTGTGAGGAGTAACTTCATCATGTGGG	2744
Db	2264	AGATCTTCCCTCCACAGAGCCTTCTTGAAAGCATGACGGAGTAACTTCATCATGTGGG	2323
QY	2745	AGAAAGTATTTGCGGGGGGAAGACACGAAATGTGATTTCAAGGCCCAAGGCCCGGCGGC	2801
Db	2324	AGAAAGTATTTCAAGGGGAGAGACATGAACTGTGATTTCAATCCCAATCGGTGGTCC	2380

```

RESULT 6
US-09-686-055A-5
; Sequence 5, Application US/09686055A
; Patent No. 6566087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OR INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67) .. (2403)
; US-09-686-055A-5

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Query Match	49.6%	Score 1787.4	DB 3	Length 3195
Best Local Similarly	86.6%	Pred. No. 0		
Matches 1971; Conservative	0	Mismatches 306	Indels 0	Gaps 0

[illegible]

Db	164	TTGTATCTGAAAGTGTATAGTGCAGAGACATGAGAAATGGCTGAAGAGAAACAACA	223
QY	645	AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAGAGGTAACAGATACGAATATGCAG	704
Db	224	AATCAGAAAGATGAATCGGCTCCTTAAGAAAGTCAGAGGTAACGAATATGCAG	283
QY	705	GAGTCGTGTACAGCTGAACAGCTACATAGACAGCGCTGGACACGGCGGGGACACCC	764
Db	284	GAGTGTGTATGAACATAACAGCTATATAGAACAAACGGTTGACACAGAGAGACACCC	343
QY	765	AACGCTCCTCTATAGGCTACGACATCATAGAGATAGGCCAATAAGCGGACGGATTGC	824
Db	344	AGCTACTCTCTATAGTAAGTGAACATCATTAATAATGACCATAAAGCCGATGGATTGG	403
QY	825	CAGTGTACTTCCTTGGAGAGTGCATATATAGCCTGTGTGTCTTATACCAACCCGGATGA	884
Db	404	CAGTGTATTTCTTGGAGAGTGCATATATAGCTGTGTATATTCACGCCACTGGGATTA	463
QY	885	AGAAAGGCCAACCCCGGCTCATCCCTGACAGGGCCCATCACCGAGGTACACATCTCTG	944
Db	464	AGAAAGGAAAAACCCGCTCATCCCTGCGGCCCATCATCAGGGACACACCGTCTCTG	523
QY	945	CCTACGTGGCCAAAGCTATAGAAAGCTGTGTGTAGAGATATCCTTGGGAGATGACAT	1000
Db	524	CTTATGTGGCCAAAGTCAGAAAAACATCTATAGAAAGACATCTTGGAGATGAACGAT	583
QY	1005	TTCTCGAGTACTGCGCTGGAAATCAGAAACCCGATCATGCTGTCTTCTTGCCCA	1060
Db	584	TTCCAAAGAGTACTGGAATCAGAAATCAGGAACTCGATCAGTCTGTTCTTGCTTACCA	643
QY	1065	TTGTCACTGCAATGTGAGACTTGATTTGGCATCTTGAACTGTACAGGCACTGGGCAAG	1120
Db	644	TTGTCACTGCAATGTGTGATTTGATATTCCTGACCTGTATCGGCACTGGGGCAAAAG	703
QY	1125	AGGCTTTTGCTCTCAGCCATCAGAGAGTTTGCAACGCCAATCTTGCTTGGGCTTCCGTA	1180
Db	704	AAGCTTCTGTCTTATAGTACCAAGAGGTGGCAACGAAATCTTGCGCTTGCAATG	763
QY	1185	CAATACACACAGGTGAGGTGTGTAGAGTCTCGCCAAACAGACGAACTGAATGACTTCC	1244
Db	764	CAATACATCAGGTGAGGTATGCAAGGCTCTTGCCAAACAGACGAATTTGAATGACTTCC	823
QY	1245	TACTGACGTATCAAAAGACATACTTTGTATTAACATAGTGGCCATAGACTCTTACTTGAAC	1300
Db	824	TACTGACGTATCAAAACATATTTTGTATTAACAATGTTGCAATAGATTCTTACTTGAAC	883
QY	1305	ACATCATGATATATGCAAAAAATCTATGTGAACGCCGACCGCTGCGGCTCTTCCAGGTGG	1360
Db	884	ACATCATGATATATGCAAAAAACCTGTGGAAATGCCGATCGTTGTGCACTTTTCCAGGTGG	943
QY	1365	ACCAACAAGAACAAAGAGCTGTACTCGACCTGTTTGACATTTGGGGAGAGAAAGAGGGA	1422
Db	944	ACCATTAAGAACAAAGAGTATATTCAGACCTTTTGTATATTTGAGAGAAAGAAAGAA	1000
QY	1425	AGCCCATCTTCAGAAAGACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTGC	1480
Db	1004	AACCTGTCTTCAAGAAAGACCAAGAGATTAAGTTTCAATTGAGAAAGAAATTTGCTGGCC	1060
QY	1485	AAGTGGCAAGAACGGCGAAGTCTTGAAACATTTCCGATGCTTACGCGAACCTCGCTTTTA	1544
Db	1064	AAGTGGCAAGAACGGGGAGTCTCTGAAACATTCAGAGTCTATGCAACCAACCCCTTTTA	1122
QY	1545	ACAGGGAGGTGGAACCTGTACACAGGCTACACAGAGAACATTCGTGTATAGCCATAG	1600
Db	1124	ACAGAGAAAGTATGATCTGTACACAGGCTACACAGCGGAAACATCTGTGCATGCCATCG	1180
QY	1605	TGAGCCGAGGACGAGTGTATGGCTGTGTGCAGATGATGAACAAGTACAGGCTATCGCTT	1660
Db	1184	TCAGCCGAGGACGAGTGTATGAGTGTGTGTGTCAGATGTCACAATAATCATGTGCACTGCTT	1244
QY	1665	TCTCAAGACAGACGAGAACATTCAGATGTTTGTGTGTCTTCTGCGCACTGGCTTTGC	1720

Db 1244 TCTTAAACAGATGAAAACAAATTCAAAATGTTGCGCTTTTGTGCTTAAACCTTAC 1303  
Qy 1725 ACTGAGTAAAGATGATACCAAGAGATCCGCCATCAGAAATGATCTACAGGGTTACCATGG 1784  
Db 1304 ACTGAGTAAATGATGATCAATAAATTCGCACTCAGAGATGATTTTACCGGGTAAAGATGG 1363  
Qy 1785 AGAAGCTTTCCTACCAAGCATCTGCACTCCGAGAGATGGCAAGGCTTCATGCGCTTCA 1844  
Db 1364 AAAAGCTGCTACCAATGATGATTTGTAATTCAGAAAGATGGCAAGGCTTCATGCAATTTCA 1423  
Qy 1845 ACTTACAGACAGCATCTGCGCGGACATAGAGCTATTCACATTTGACATTTGGCTTTGG 1904  
Db 1424 CCGTTCGCCGTGCTCTGCAAGAAATTTATTTTCACTTTGACATTTGGCTTTGG 1483  
Qy 1905 AGAAGATGAGGCTGGGATCTTTGTCTACATGATCCATGCGTCTTTGGGACATCTCTTT 1964  
Db 1484 AAAACATGAGGCTGGGATTTTGTCTACATGATCCATGCGTCTTTGGGACATCTCTGT 1543  
Qy 1965 TTGAACCTGAAAAATTTGCGCTTTTATCATGCTGTGAAAGAAATCTATCGCGGGTTTC 2024  
Db 1544 TTGAGCTTAAAAAGTTGTGCGTTTATTTATGCTGTGAAAGAAATCTATCGCGGGTTTC 1603  
Qy 2025 CTTTACCAAACTGGAAGCATGCAAGTCAAGGTGCAACATGATATGCAATCTTCAAA 2084  
Db 1604 CTTATCAAACTGGAAGCATGCGGTCACTGTACACAATGCAATGTATGCAATCTTCAAA 1663  
Qy 2085 AACAAAGATGGCTCTTCAAGACCTGAGAGGCAAGGCGCTGTAATTTGCGTCTGTGCC 2144  
Db 1664 AACATCAACGCTTTTCAAGACCTTGAAGGCAAGGCGCTGTAATTTGCGTCTGTGC 1723  
Qy 2145 ATGACCTGGAACAAGGGCTTTCAGTAAACAGTAACTGTGCAAGATTTGCAACACCCCTG 2204  
Db 1724 ATGACCTGGAACAAGGGCTTTCAGTAAACAGTAACTGTGCAAGATTTGCAACACCCCTG 1783  
Qy 2205 CCGCGCTGATCTCACTTCCACATGGAAGAACCACTTCTCCCAAGCGGTTCATCC 2264  
Db 1784 CCGCTCTTACTCCTCACTTCCACATGGAAGAACCACTTCTCCCAAGCGGTTCATCC 1843  
Qy 2265 TTCAGCTGGAAGGCAAAATATCTTCCACCGTGAAGCTCCAGAGATGCAAGAGGTGC 2324  
Db 1844 TTCAGCTGGAAGGCAAAATATCTTCCACCGTGAAGCTCCAGAGATGCAAGAGGTGC 1903  
Qy 2325 TGGAGATCAATCCGCAAGCCATCATGCGCAACGACCTCGCTTATTTTGGGAACAGA 2384  
Db 1904 TGGAGATCAATCCGCAAGCCATCATGCGCAACGACCTCGCTTATTTTGGGAACAGA 1963  
Qy 2385 AGCAGTTGGAAGAGATGATCAAGACAGGGTGCCTGAACCTTCCACACAGTCCCATGAG 2444  
Db 1964 AGCAGTTGGAAGAGATGATCAAGACAGGGTGCCTGAACCTTAAATCAATCACTATGAG 2023  
Qy 2445 ACCGTGTCAATCCGCTTGAATGATGATGCTGCTGTGATCTTTGCTGTGACCAAACTATGG 2504  
Db 2024 ACCGTGTAAATTTGTTGATATGATGATGCTGCTGTGATCTTTGTTCTGTACAAAACTGTGGC 2083  
Qy 2505 CAGTTTAAAAATTTGACAGCAATGATATATATGAGAAATTTCTGGGCTGAGGGTATGAGA 2564  
Db 2084 CCGTTTAAAAATTTGACAGCAATGATATATATGAGAAATTTCTGGGCTGAGGGTATGAGA 2143  
Qy 2565 TGAAGAACTGGGCAATCAAGCCATCTTATGATGACAGAGACAAAGCAAGATGAATCC 2624  
Db 2144 TGAAGAAATTTGGGAATCAGGCTATCTTATGATGACAGAGACAAAGATGAATCC 2203  
Qy 2625 CTGAAGGCAAGCTGCAATTTCAAAATGCTGTGCAATTCCTGTCTATACCACTTGAAGC 2684  
Db 2204 CCAAGGCAAGCTGCAATTTCAAAATGCTGTGCAATTCCTGTCTATACCACTTGAAGC 2263  
Qy 2685 AGATCTCTCCCAACCAAGAGCTCTGTGTAAGGCTGCAAGGATTAACCTCAATGAGGG 2744  
Db 2264 AGATCTCTCTCCCAACCAAGAGCTCTGTGTAAGGATTAACCTCAATGAGGG 2323  
Qy 2745 AGAAGTAAATTTGCGGGGAGAGACAGCAATGTTGATTTTCAAGGCTTCAAGCCGCGC 2801  
Db 2324 AGAAGTAAATTTGCGGGGAGAGACAGCAATGTTGATTTTCAATCCCATCTGTGGCTC 2380

RESULT 7  
US-09-420-190-2  
; Sequence 2, Application US/09420190  
; Patent No. 6673564  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana  
; APPLICANT: Hunter, John Joseph  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: Methods for using 22045, A Human Cyclic  
; TITLE OF INVENTION: Nucleotide Phosphodiesterase  
; FILE REFERENCE: 5800-71  
; CURRENT APPLICATION NUMBER: US/09/420,190  
; CURRENT FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 4381  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (67)...(2403)  
US-09-420-190-2  
  
Query Match 49.6%; Score 1787.4; DB 3; Length 4381;  
Best Local Similarity 86.6%; Pred. No. 0;  
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;  
  
Qy 525 GTTTGACGATGAAAAAGGAGGCGCTATCTTCTCCATCCCGAGTATTAGTAAT 584  
Db 104 GTTTGACGATGAAAAAGGAGGCGCTATCTTCTCCATCCCGAGTATTAGTAAT 163  
Qy 585 TTGTTCTGAAAGTGTAGTGCAGAGCTGTGAAAAAGTGTGTAAGGAAAAACCAACA 644  
Db 164 TTGTTCTGAAAGTGTAGTGCAGAGCTGTGAAAAAGTGTGTAAGGAAAAACCAACA 223  
Qy 645 AAGCAAAAGTGAACCATCTCCCAAGAAAGTCAAGGATCCAGATTAAGATTTGACG 704  
Db 224 AATCAAGATGAATGCGCTCTTAAGAAAGTCAAGGATCCAGATTAAGATTTGACG 283  
Qy 705 GAGTGTGACAGCTGGAACAGTATAGAGAGGCGCTGACAGGGGCGGGAACAAC 764  
Db 284 GAGTGTGATATGAATGAACGATATATGAACAAGTTGACAGAGAGAGACAAC 343  
Qy 765 ACCTGCTCCTTATGAGCTCAGAGCATCATAGATAGCCAAAGCCGAGATTTG 824  
Db 344 AGCTTACTCTTATGAACTGAGCATCATTAATAATAGCAAAAAGCCGATGATTTG 403  
Qy 825 CACTGTAATCTTCTGGAAGATGATTAATAGCTGTGTGTTCATACACCCGGGATGA 884  
Db 404 CACTGTAATTTCTTGGAGATGCAATATAGCTGTGTATATCAAGCCACTGGGATTA 463  
Qy 885 AGAAGGCAACCCCGGCTATCCCTGCAAGGCGCAATCCAGGGATACACCATCTGT 944  
Db 464 AGAAGGAAAAACCCCGCTCATCTGTGCGGCCCATCATCAGGGACCAACCTGTCTG 523  
Qy 945 CTAAGTGGCAAGTCTAGGAACGTTGTTGTAGAGATATCTTTGGGATGAGCGAT 1004  
Db 524 CTTATGTGGCAAGTCCAGAAAACACTGCTATTAAGAACATCTTTGGATGAGAT 583  
Qy 1005 TTCTGAGGTAATGCGCTGGAATCAGAAACCGCATCCAGTCTGTTTCTTGGCCCA 1064  
Db 584 TTCCAAAGGTAATGCACTGGAATCAGGAGCTGTATCCAGTCTGTTCTTATCAAA 643  
Qy 1065 TTGTCACTGCAATTTGAGAGATTTGATGAGCATCTGTGAACGTGCAAGGCACTGGGGCAAG 1124  
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Qy 1125 AGGCTTCTGCTCAGGCATCAGAGGTTGCAACAGCCATCTTGTGGCTTCCGTAG 1184  
Db 704 AAGCTTCTGTCTTATGATCAACAGAGGTTGCAACAGCAATTTTGGCTTCACTAG 763



QY 1185 CAATACACGAGGTGAGGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCC 1244  
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 QY 1245 TAATCGACGTATCAAGACATATCTTGTATACATAGTTCATAGACTCTTACTTGAAC 1304  
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 DB 884 ACATCATGTATATGCAAAAATCTGTAAGTCCGATGTTGTGCACTTTTCCAGGTG 943  
 QY 1365 ACCACAAAGAACAGAGCTGTACTCGGACCTGTTTGCATTTGGGAGAGAGAGGGA 1424  
 DB 944 ACCATTAAGAACAGAGATTAATTAAGACCTTTTGTATTTGAGAGAGAGAGAGAG 1003  
 QY 1425 AGCCCATCTTCAAGAACACCAAGAGATCAGATTTTTCATTAAGAAAGGATTTGCTGTC 1484  
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 QY 1485 AAGTGGCAAGAACAGGCGAAGTCTTGAAGATCCGATGCTTACCGGAGCCCTCGCTTTA 1544  
 DB 1064 AAGTGGCAAGAACAGGCGAAGTCTTGAAGATCCGATGCTTACCGGAGCCCTCGCTTTA 1123  
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 DB 1304 ACTGTGCTTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1363  
 QY 1785 AGAAGCTTTCTTACCAAGACATCTGCACTCCGAGAGATGAGAGGCTTCACTGCGCTTCA 1844  
 DB 1364 AGAAGCTGCTTACCAAGACATCTGCACTCCGAGAGATGAGAGGCTTCACTGCGCTTCA 1423  
 QY 1845 ACCTAACAGACAGCATCTGCGCGGACATGAGACTATTCATCTTGAACATTTGCTTCTTGC 1904  
 DB 1424 CCCTTCCGCTGCTCTGCAAGAAATTTGAATTTTCCATTTGACATTTGCTTCTTGC 1483  
 QY 1905 AGAATCATGAGCTGGGATCTTTGTCTATCATGATCATGCTTGTGGGACATCTGCTT 1964  
 DB 1484 AGAATCATGAGCTGGGATCTTTGTCTATCATGATCATGCTTGTGGGACATCTGCTT 1543  
 QY 1965 TTGAACTTGAAGAAATTTGCTCTTATCATGCTGTGGAAGAACTATTCGCGCGGTTCC 2024  
 DB 1544 TTGACTTGAAGAAATTTGCTCTTATCATGCTGTGGAAGAACTATTCGCGCGGTTCC 1603  
 QY 2025 CTTTACCAACCTGGAAGCATGAGTCAAGGTGCACTGCACTGATGTAATGCAATCTTCAA 2084  
 DB 1604 CTTTACCAACCTGGAAGCATGAGTCAAGGTGCACTGCACTGATGTAATGCAATCTTCAA 1663  
 QY 2085 ACAACATGAGCTCTTCAACAGACTCGAGCGCAAGGCTGCTAATTTGGGTCTGTGTC 2144  
 DB 1664 ACAACATGAGCTCTTCAACAGACTCGAGCGCAAGGCTGCTAATTTGGGTCTGTGTC 1723  
 QY 2145 ATGACCTGGAACCAAGGCGCTTCACTAAGCTACCTGCAAGATTTGCAACACCCCTGTC 2204  
 DB 1724 ATGACCTGGAACCAAGGCGCTTCACTAAGCTACCTGCAAGATTTGCAACACCCCTGTC 1783  
 QY 2205 CGGCGCTGTACTCTCACTCTCAACATGAGAGCAACCACTTCTCCAGAGCGGTCTCATTC 2264  
 DB 1784 CGGCGCTGTACTCTCACTCTCAACATGAGAGCAACCACTTCTCCAGAGCGGTCTCATTC 1843

QY 2265 TTCAGCTGAAGGCGACATATCTTCTCCACCCTGAGCTCCAGCGAGTACAGACAGGTGC 2324  
 DB 1844 TTCAGTTGGAAGGCGACATATCTTCTCCACCCTGAGCTCCAGGTATATGAGCAGGTGC 1903  
 QY 2325 TGGAGATCATCCGCAAGCCATCATGCGCACGACCTCGCCCTATATCTTTGGGAACAGGA 2384  
 DB 1904 TTTGATCATTCGCAAGCCATCATTTGCGCACGACCTTGTATATCTTTGGAACAGGA 1963  
 QY 2385 AGCAGTTGAGAGATGTAACAGACAGGAGCTGTAACCTCCACACAGAGTCCCATGAG 2444  
 DB 1964 AGCAGTTGAGAGATGTAACAGACAGGAGCTGTAACCTCCATATATATCATATGAG 2023  
 QY 2445 ACCGTGTACGCTGTATGATGATCTGCTGTGATCTTTGCTGTGACCAAACTATGAGC 2504  
 DB 2024 ACCGTGTATTTGTTGATGATGATCTGCTGTGATCTTTGTTCTGTGACAAACTGTGCG 2083  
 QY 2505 CAGTTTCAAAATTTGACAGCGAATGATATATGCAAAATTTCTGGCTGAGGCTGATGGA 2564  
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 QY 2565 TGAAGAGCTGGGCAATACAGCCATTTCTATGATGAGACAGAGACAAAGCGAGATGAAGTCC 2624  
 DB 2144 TGAAGAAATTTGGAAATACAGCTTATTTCTATGATGAGACAGAGACAAAGAGATGAAGTCC 2203  
 QY 2625 CTCAAGGCAAGCTCGAATTTCTAATGCTGTGCAATTCCTGCTATACCACTTGAAGC 2684  
 DB 2204 CCAAGGCAAGCTTGTGTTCTAATGCTGTGCAATTCCTGCTATACCACTTGAAGC 2263  
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 DB 2264 AGATCTTCCCTCCACAGAGCTCTTGTGGAAGGATGAGGAGATTAATCTCATGCTGAGG 2323  
 QY 2745 AGAAGTAATTCGCGGGAAGAGACAGCAATGTAATTTCAAGGCCAGGCCGCGGC 2801  
 DB 2324 AGAAGTAATTCGAGGGAAGAGAGACTGCAACTGGAATTTCAATCCCATCCGCTGCTC 2380

RESULT 8  
 US-08-951-648-1  
 ; Sequence 1, Application US/08951648  
 ; Patent No. 5932465  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loughney, Kate  
 ; TITLE OF INVENTION: Phosphodiesterase 8  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker, Sears Tower Suite 6300  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: US  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/951,648  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Williams Jr., Joseph A.  
 ; REGISTRATION NUMBER: 38,659  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-0448  
 ; TELEFAX: 312-474-0448  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2298 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single



TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..2298  
 OTHER INFORMATION:  
 OTHER INFORMATION: /note="The amino acid encoded by nucleotides 868-870 is  
 OTHER INFORMATION: either Pro or Lys."  
 US-08-951-648-1

Query Match 49.5%; Score 1785; DB 2; Length 2298;  
 Best Local Similarity 86.5%; Pred. No. 0;  
 Matches 1968; Conservative 1; Mismatches 306; Indels 0; Gaps 0;

QY 527 TTGACGATGAAAAAGGTGAAGGCTATCTTTCTCTCCATCCCGAGTATTAGTGAATTT 586  
 DB 1 TTGACGATGAAAAAGGTGAAGGCTATCTTTCTCTCCATCCCGAGTATTAGTGAATTT 60  
 QY 587 GTTCTGAAAAGTGTAGTGAAGACTGTGAAAAAGTGTGAAGAGAAAAACAACAA 646  
 DB 61 GATATGAAAAGTGTAGTGAAGACTGTGAAAAAGTGTGAAGAGAAAAACAACAA 120  
 QY 647 GCAAAAGATGAACCATCTCCCAAGAAAGTCAAGAGGTAACGAGATACGAATATGCAAGGA 706  
 DB 121 TCAGAAAGATGAATCGGCTCTCTAAGAAAGTCAAGAGGTAACGAGATACGAATATGCAAGGA 180  
 QY 707 GTCGTGACGAGCTGAACAGCTACATAGAGACGCGCTGGAACGCGCGGGAACAACAC 766  
 DB 181 GTTGTATATGAACTTAACAGCTATATAGAACAGCGTGGACACAGAGAGAACACACAG 240  
 QY 767 CTGCTCTCTATAGAGCTCAAGACGATCATCAGATAGACCAAAAGCCGACGATTTGCA 826  
 DB 241 CTATCTCTATAGAGCTCAAGACGATCATTAATAATAGCCAAAGCCGATTTGCA 300  
 QY 827 CTGTACTCTTGTGAAGAGTCAATTAAGCTGTGTGTCTTATACACCCCGGAGTGAAG 886  
 DB 301 CTGTATTTCTTGTGAAGAGTCAATTAAGCTGTGTGTCTTATACACCCCGGAGTGAAG 360  
 QY 887 GAAGGCAACCCCGGCTCATCCCTGCAAGGCGCCATCAACCGAGGTACCAACATCTCGCC 946  
 DB 361 GAAGGCAACCCCGGCTCATCCCTGCGGCGCCATCACTCAAGGCAACACCGTCTCGCT 420  
 QY 947 TACGTGGCCAAGTCTAGGAAGACGTTGTTGTAGAGATATCTTGGGAGTGAACGATTT 1006  
 DB 421 TATGTGGCCAAGTCTAGGAAGACGTTGTTGTAGGAACATCTTGGAGTGAACGATTT 480  
 QY 1007 CCTGAGAGTATGCGCTGTGAATCAGAAACCCGATCCAGTCTGTCTTCTTCTGCCATTT 1066  
 DB 481 CCAAGAGTATCTGAGCTGGAATCAGGGACTGTATCCAGTCTGTCTTCTTACCAATTT 540  
 QY 1067 GTACATGCCATTGGAAGCTTGAATTGGCATCTTGAACTGTACAGGCACTGCGGCAAAAG 1126  
 DB 541 GTACATGCCAATTGGTAGCTTGAATTGGTATCTGAGCTGTATCGGCACTGCGGCAAAAG 600  
 QY 1127 GCCCTTCTGCTCAAGCCATCAGAGGTGCAACAGCCATCTTGTGCGCTTCCGTAACA 1186  
 DB 601 GCCCTTCTGCTTATGTAACAGAGGTGCAACAGCAAAATCTTGTGCGGCTTCAATGTA 660  
 QY 1187 ATACACCAAGGTGAGGTGTGTAGAGTCTGCGCAACAGACCGAACTGAATGACTTCTTA 1246  
 DB 661 ATACATCAAGGTGAGGTGTGTAGAGTCTGCGCAACAGACAGAAATGAAATGACTTCTTA 720  
 QY 1247 CTGAGAGTATCAAGACATCTTGAATACATAGTTGSCATAGACTCTCTACTTGAACAC 1306  
 DB 721 CTGAGAGTATCAAAACATCTTGAATACATAGTTGSCATAGACTCTCTACTTGAACAC 780  
 QY 1307 ATCATGATATATGCAAAAAATCTAGTGAACGCGACCGCTGCGCTCTTCCAGGTGAC 1366  
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 QY 1367 CACAGAAACAAAGAGCTGTACTCGGACTGTGTTTGAATTTGGGAGAGAAAGAGGGGAG 1426  
 DB 841 CATTAAGAAACAAAGAGTATATTCAGACCTTTTGTATTTGGAGAGAAAGAGGAGAAA 900

QY 1427 CCCATCTTCAAGAACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTCAA 1486  
 DB 901 CCTGTCTTCAAGAAACCAAGAGATTAAGATTTTCAATTGAGAAAGGATTTCTGCGCAA 960  
 QY 1487 GTGGCAAGAACAGGGAAGTCTTGAACATTCGCGATGCTTACGCGGACCTTGCTTTAAC 1546  
 DB 961 GTAGCAAGAACAGGGAAGTCTTGAACATTCGAGATGCTTATGCAAGCCCAAGCTTTAAC 1020  
 QY 1547 AGGAGGTGAGCTGTACACAGGCTACACCAAGAGAACATTTCTGTATATGCCATATG 1606  
 DB 1021 AAGAAAGTATGACTTGTACACAGGCTACACCAAGGAAATCTCTGTGACATGCGCATCTG 1080  
 QY 1607 AGCCGAGGAGCGGTATTTGCGTGTGCGAGATGTGACACAAATACAGCGGTATGCGCTTC 1666  
 DB 1081 AGCCGAGGAGCGGTATTTGCGTGTGCGAGATGTGACACAAATATCAGTGCAGTCTTTC 1140  
 QY 1667 TCCAAAGACAGAGAACAACTTCAAGATGTTGCTGTCTTGTGCGCACTGCGCTTGAC 1726  
 DB 1141 TCTAAACAGATGAABAAACATTTCAAAATGTTTGCCTTTTGTGTCTTATAGCTTACAC 1200  
 QY 1727 TGTGCTAACATGTACCAAGATCCGCCACTCAAAATGATCTACAGGTTACATGAG 1786  
 DB 1201 TGTGCTAACATGTATCATAGAAATGCGCACTCAGAGTCAATTTACCGGGTAAAGATGAA 1260  
 QY 1787 AAGCTTCTTACCAAGCATCTGACCTCCGAGAGTGGCAAGGCTCATGCGCTTCAAC 1846  
 DB 1261 AAGCTTCTTACCAATGACATTTGTACTTCAAGAGATGGCAAGGCTCATGCAATTCACC 1320  
 QY 1847 CTACAGACAGCATCTGCGGGGACATGAGCTATTCCATTTGACATTTGGTCTTTCGAG 1906  
 DB 1321 CTTCCTGCGGCTCTGCAAAAGAAATTTGAATTTATTCATTTGACATTTGGTCTTTCGAA 1380  
 QY 1907 AACATGTGCTGAGATCTTGTGTACATGATTCATCGTCTTGTGGAACATCTGTTT 1966  
 DB 1381 AACATGTGCTGAGATTTTGTGTACATGATTCATCGGCTCTGAGGACATCTGCTTT 1440  
 QY 1967 GAACTTGAABAAATTTGCGGCTTTATCATGTCTGTGAAGAAACATTAATGCGGCTTCT 2026  
 DB 1441 GAGCTTGAABAAATTTGCGGCTTTATCATGTCTGTGAAGAAACATTAATGCGGCTTCT 1500  
 QY 2027 TACCAACATGGAAGATCAGTCAAGTGGGCACTGCAATGTATGCAATCTTCAAAAC 2086  
 DB 1501 TATCAACATGGAAGATGCGGCTGATGACATGTATGCACTGCAATGTATGCAATCTTCAAAAC 1560  
 QY 2087 AACATGAGCTCTTCAAGACCTGAGCGCAAGGCTCTTATGCGTGTCTGTCAT 2146  
 DB 1561 AACATGAGCTCTTCAAGACCTGAGCGCAAGGCTCTTATGCGTGTCTGTCAT 1620  
 QY 2147 GACCTGAGCAACAGGGCTTCAAGTACAGTACCTGCAAGTTCACACCCCTGCGG 2206  
 DB 1621 GACCTGAGCAACAGGGCTTCAAGTACAGTACCTGCAAGTTCACACCCCTGCGG 1680  
 QY 2207 GCGCTGTATCTCCACTTCCACATGAGGCAACCACTTCCCGAGCGGTCATCTT 2266  
 DB 1681 GCTCTGTATCTCCACTTCCACATGAGGCAACCACTTCCCGAGCTGTCTCATCTTC 1740  
 QY 2267 CAGCTGAAAGGCACAATATCTTCCACCTGAGCTCCAGCGAGTACGAGAGTGTCTG 2326  
 DB 1741 CAGTGTGAAGGCACAATATCTTCTCACTGTAGGCTTCAGTGAATATGAGAGGTGCTT 1800  
 QY 2327 GAGATCATCGCAAGCCATGATCGCAACCGACTGCGCTTATATCTTTGGAAACAGAGAG 2386  
 DB 1801 GAGATCATCGCAAGCCATGATCGCAACCGACTGCGCTTATATCTTTGGAAACAGAGAG 1860  
 QY 2387 CAGTTGAGAGATGTATCCAGAGAGGTGCGCTGAACCTTCCAAACAGATCCCATTCAGAC 2446  
 DB 1861 CAGTTGAGAGATGTATCCAGAGAGGTGCGCTGAACCTTCCAAACAGATCCCATTCAGAC 1920  
 QY 2447 CGTGTATCGGCTTGTATGATGATCTGCGCTGTATCTTGTCTGTGACAAATCTGTGCGCA 2506  
 DB 1921 CGTGTATCGGCTTGTATGATGATCTGCGCTGTATCTTGTCTGTGACAAATCTGTGCGCC 1980

Qy	2507	GTTCAAAATTTGACAGCGAATGATATATATATGACAAATTCCTGGGCTGAGGGGATGAGATG	2506
Dp	1981	GTTCAAAATTTGACAGCGAATGATATATATGACAAATTCCTGGGCTGAGGGGATGAAATG	2040
Qy	2567	AAGAAGCTGGGCATACAGCCCATTCCTTGAATGACAGAGACAAGCGAGATGAAGTCCCT	2626
Dp	2041	AAGAATTTGGGAATACAGCTATTCTCTATGATGACAGAGACAAGAAAGGATGAAGTCCCC	2100
Qy	2627	CAAGGGCAGCTGGATTTCTTACAATGCTGTGGCCATTCCTGCTATACACTTGAACCGAG	2686
Dp	2101	CAGAGCAGCTTGGTTCTTACAAATGCGTCGTGCACATTCCTCTATACACCCTTACCCAG	2160
Qy	2687	ATCTCTCCCAACCAAGAGCTCTGTGTGAAGCCTGACGGATTAACCTCAATCAGTGGGAG	2746
Dp	2161	ATCTCTCCCTCCACAGAGCTCTTCTGTAAACATGACGAGATTAATTCAGTCAATGGGAG	2220
Qy	2747	AAGGTAATTCGCGGGGAAGAGACAGCAATGTGATTTCAAGCCCAAGGCGCGGCGC	2801
Dp	2221	AAGGTGATTTCAAGGGAGAGAGACTGCAACCTGGAATTTCAATCCCATCGTGGCTC	2275

[illegible]

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RESULT 9
US-09-174-437-1
; Sequence 1, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2298)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (868)..(870)
; OTHER INFORMATION: The amino acid encoded by nucleotides 868-870 is
; OTHER INFORMATION: either Pro or Leu
; IS-09-174-437-1

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Db	601	GCCTTCTGTCTTAGTCAACGAGAGTTGGACAGAGAAATCTTGCGGTTCAGTAGA	660
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Db	721	CTGCACGTAATAAAAAACATAATTTTGATATACATAGTGGCAATATGATCTCTACTTAAAC	780
Qy	1307	ATCATGATATATATGCAAAAAATCTAGTAGAACGCCGACCGCTGCGGCTCTTCCAGGTGCAC	1366
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Qy	1367	CACAGAACAGAGAGCTGTACTCGGACCTGTTTGCATTTGGGGAGAGAAAGAGGGGAAG	1422
Db	841	CATAGAGAACAGAGAGTTATATTACAGACCTTTTGATATTTGGAGAGAAAGAAAGGAAAA	900
Qy	1427	CCCATCTTCAAGAAAGACCAAGAGATCAGATTTTCCATTGTAGAAAGGATTTCTGTGTCA	1488
Db	901	CCCTGTCTTCAAGAAAGACCAAGAGATAGATTTTCAATTGTAGAAAGGATTTGTGCGCCA	960
Qy	1487	GTGCAAGAAAGAGCGAAGTCTTGAAACAATTCGAGTGGCTGAGGAGCCCTGCGTTTAAAC	1544
Db	961	GTACCAAGAAAGAGGGGAAGTCTTGAACATTTCCAGATGCTATGACAGACCCACGCTTTAAC	1022

Query Match	49.5%;	Score 1785;	DB 3;	Length 2298;
Best Local Similarity	86.5%;	Pred. No. 0;		
Matches 1968;	Conservative 1;	Matches 306;	Indels 0;	Gaps 0;
QY	527	TTGACGGATGAAAAGGTGAAGCCGCTATCTTCTCTCCATCCCGAGGTATTAGATGAATTT	586	
Db	1	TTGACAGATGAAAAGTGAAGGCATATCTTCTCTCACCCGAGATTATGATGAATTT	60	
QY	587	GTTCCTGAAAGTGTATGTCAGAGACTGTGAAAAGTGCTGAAGAGGAAAACCAACAA	646	
Db	61	GTATCTGAAAGTGTATGTCAGAGACTGTGAAAAGTGCTGAAGAGGAAAACCAACAA	120	
QY	647	GCAAAAGATGAACCATCTCCCAAGAAAGTCAGCAGTACCAAGATTACGAATATGTCAGGGA	706	
Db	121	TCAGAAAGATGAATGGGCTCTTAAGGAAAGTCAGCAGTACCAAGATTACGAATATGTCAGGGA	180	
QY	707	GTCTGTATACGAGCTGGAACAGTATATGAGCAGCGCTTGACACAGCGCGGGGACACACAC	766	
Db	181	GTTGTATATGAACCTAAACAGCTATATATGAAACAAACGGTTTGACACAGAGGAGAACACAG	240	
QY	767	CTGCTCTCTTATAGCTCAGCAGCATATCATCAGGATAGCCACAAAAGCCGACGATTTTGCA	826	
Db	241	CTACTCTCTTATAGCACTGAGCAGCATATTAATAATAGCACAAAAGCCGATGATTTTGCA	300	

Qy	1607	AGCCGAGCGACCTGATTTGCGGTGGTGAGATGCGTAA	CAAGATCAGCGTAGCCCTTTC	1666
Db	1081	AGCCGAGCGACCGTGAATGATGTGTGGTGAATGTC	CAACAAATAGTGGCAGTGTCTTTC	1144
Qy	1667	TCCAAGACAGACGAAACACTTCAAGATGTTTGCTGTTCTGCGC	ACTGGCCTTTCGAC	1722
Db	1141	TCTAAACAGATGAAACCACTTCAAAATGTTGGCGCTCTTTGCGCTT	TATAGCCTTACAC	1200
Qy	1727	TGTGCTAACATGTATACCAAGATTCGGCACTCAGAAATGCA	ATCTACAGGGTTAACATGGAG	1788
Db	1201	TGTCTAATATGTTATCATAGAAATTCGCACATCAGATGCA	ATTTACCGGGTAAACGATGGAA	1266
Qy	1787	AAGCTTTCCTAACCAACAGATCTGCACTCCGAGAGTGGCAAGG	CTCATGGCGTTTCAAC	1844
Db	1261	AAGCTGTCTCAACCATAGCATTTTGTATCTTCAAAAGATGGCAAGG	CTCATGCAATTTTCAAC	1322
Qy	1847	CTACACAGCGCATCTGCGCGGAGATCGAGCTAATTC	CACTTGTGA	1906
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Db	1381	AAATGTGGCTCGGAATTTTGTGTCATAGTTCATCGGTCGTGGAGATCCCTGCTT	1440
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Db	1621	GACCTGGACCAAGAGGCGTTCAGTAAAGCTACGTGACGAAGTTGCAACCAACCCCTGCGC	1680
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Db	1681	GCTCTTAATCTCACTTCACCACTGAGACAGCACTTCCTCCAGACTGTGTCCATCTTC	1740
Qy	2267	CAGCTGGAAGGGCAATATTTCTTCCACCTTGAGCTCCAGCGGTACAGACAGTGTCTG	2326
Db	1741	CAGTTGGAAAGGGCAATATCTTCTTCCACCTTGAGCTCCAGTGAATGAGCAAGTGTCTT	1800
Qy	2327	GAGATCAATCCGCAAGGCATCATGCGCCACGACCTCGGCTCTATCTTTGGGAACAGGAAG	2386
Db	1801	GAGATCAATCCGCAAGGCATCATCTTGGCCACAGACTTGTGTTATATCTTTGGAAAACAGGAAG	1860
Qy	2387	CAGTTGGAGAGATGTACCAAGAGGGTCGTGAACCTTCCAAACAACAGTCCCATTCAGAC	2446
Db	1861	CAGTTGGAGAGATGTACCAAGCGGATCACTAAACCTTAATATCAATCAATGAGAC	1920
Qy	2447	CGTGTCAATCGGCTTGATGATGACGCGCGTGTATCTTTGCTGTGACCAACTATGAGCA	2506
Db	1921	CGTGTAAATGGATTGATGATGATGACGCGCGTGTATCTTTGCTGTGACCAACTGTGGCC	1980
Qy	2507	GTTACAAATTTGACAGCGAATGATATATATGACAAATTCGAGGCTGAGAGGTGATGATG	2566
Db	1981	GTTACAAATTTGACAGCGCAATGATATATGAGAAATTCGAGGCTGAGAGGTGATGATG	2040
Qy	2567	AAGAACTGGGCAATACAGCCCATTTCTATGATGACAGAGCAAGCGAGATGAAGTCCCT	2626
Db	2041	AAGAAATTTGGGAATACAGCCCTATTCCTATGATGACAGAGCAAGAAAGATGAAGTCCCT	2100
Qy	2627	CAGGGGCAAGCTTGGATTCATCAATGCGCGTGGCATTTCCCTGTATCAACCTTACCGAG	2686
Db	2101	CAGGGCAAGCTTGGATTCATCAATGCGCGTGGCATTTCCCTGTATCAACCTTACCGAG	2160
Qy	2687	ATCTCTCCCAACCAAGAGCTTCGTGTGAAGGCTGCAAGGATTAACCTCAATCATGTGGAG	2746
Db	2161	ATCTCTCTCCCAACGAGGCTTCCTTGTGAAGGATGCAAGGATTAATCTCAGTCAGTGGAG	2220
Qy	2747	AAGGTAAATTCGCGGGGAAAGACACAGCAATGTGATTTCAAGGCCCAAGGCCCGGCCG	2801
Db	2221	AAGGTAAATTCAGGGGAAAGACTGCAACCTGGAATTTCAATCCCAATCGTGTCTC	2275

RESULT 10  
 US-09-686-055A-1  
 ; Sequence 1, Application US/09686055A  
 ; Patent No. 6565087  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Loughney, Kate  
 ; TITLE OF INVENTION: Phosphodiesterase 8A  
 ; FILE REFERENCE: 21866/35047  
 ; CURRENT APPLICATION NUMBER: US/09/686,055A  
 ; CURRENT FILING DATE: 2000-10-11  
 ; PRIOR APPLICATION NUMBER: 08/951,648  
 ; PRIOR FILING DATE: 1997-10-16  
 ; NUMBER OF SEQ ID NOS: 48

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(2298)
; NAME/KEY: misc feature
; LOCATION: (866)..(870)
; OTHER INFORMATION: The amino acid encoded by nucleotides 868-870 is
; OTHER INFORMATION: either Pro or Leu
US-09-686-055A-1

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Query Match	49.5%;	Score 1785;	DB 3;	Length 2228;
Best Local Similarity	86.5%;	Pred. No. 0;		
Matches 1968;	Conservative	1;	Mismatches 306;	Indels 0;
			Gaps	0;
QY 527	TTGACGGATGAAAGGTGAAGGCCCTATCTTCTCTCCATCCCCAGGTATTAGATGAATTT	586		
DB 1	TTGACAGTGAAGAAAGTGAAGCATATCTTCTCTTCACCCCAGGTATTAGATGAATTT	60		
QY 587	GTTCCTGAAAGTGTTAATGCAAGACCTGTGAAAAAGTGGCTGAAGAGAAAAACCAACAA	646		
DB 61	GTATCTGAAGATGTTAATGCAAGACAGTAGAGAAATGGCTGAAGAGAAACCAACAA	120		
QY 647	GCAAAAGATGAACCATCTCCCAAGAAAGTCAGCGGTATCCAGGATTAAGATTATGCAAGGA	706		
DB 121	TCAGAAAGTGAATCGGCTCTTAAGAAAGTCAGCGGTATCCAGGATTAAGATTATGCAAGGA	180		
QY 707	GTGCGTATCGAGCTGAACAGCTATATAGCAGCGGCTTGACACGGCGGGGCAACACAC	766		
DB 181	GTGTATATGTAACCTAAACGCTTATATAGAACACAGGTGACACAGAGAGAACAAACAG	240		
QY 767	CTGCTCCTCTATGAGCTTCAGCAGCATATCAAGATAGCCCAAAAGCTGACGATTTGCA	826		
DB 241	CTACTCCTCTATGAACTGAGCAGCATATTAATTAATGACAAAGACGATGATTTGCA	300		
QY 827	CTGTATCTTCTTGAGAGTGCATATATATAGCTGTGTGTGTTCATATCCACCCGGGATGAG	886		
DB 301	CTGTATTTCTTTGGAGAGTGCATATATATAGCTGTGTATATTCACGCCACTGGGATTAAG	360		
QY 887	GAAAGCCCAACCCGGGCTCATCCCTGCAAGGGGCCATCAACCAAGGGTACCAACATCTGACC	946		
DB 361	GAAAGAAAACCCCGCTCATCCCTGCTGGGCCCATCACTCAGGGCACCAACGCTCTGCT	420		
QY 947	TACGTGCGCAAGTCTAGAGAGACGTTGTGTAGAGATATCTTTGGGATGAGCGATTT	1006		
DB 421	TATGTGGCCAACTCAGAGAAACACTGCTATTAAGAGACATCTTTGAGATGAACGATTT	480		
QY 1007	CCTCAGAGTACTGGCTGTAATCAAGAAACCCGCATCCAGTCTGTTCTTGTGCTGCCATT	1066		
DB 481	CCAAAGAGTATCGAATCGAATCAAGGGACTGTATCCAGTCTGTTCTTGTCTTACCAATT	540		
QY 1067	GTCACTGCCATTGAGAGACTTGAATGGCATCCTTGAACGTATCAAGGCACTGGGGCAAAAG	1126		
DB 541	GTCACTGCAATTTGTGACCTTAATGTGATTCCTGAGCTGTAATCGGCACTGGGGCAAAAG	600		
QY 1127	GCTTCTGCGCTCAGGCATCAGAGGTTGCAACAGCCAACTTGTCTTGGACTTCCGTAGCA	1186		
DB 601	GCTTCTGTCTTATGTCACAGAGAGTTGCCAACAGCAATCTTGGCTTGAGTACGATAGCA	660		
QY 1187	ATACACCAAGTGCAGGTGTGTAAGAGTCTCGCAACAGACCGAACTGAATGACTTCTTA	1246		
DB 661	ATACATCAAGTGCAGGTATGCAAGAGGCTTGTCCAAACAGACAGATTAATGAATTTCTTA	720		
QY 1247	CTGACAGTATCAAAACATCTTTGATATACATAGTGCATATGACTCTTATGAAACAC	1306		
DB 721	CTGCGAGTATCAAAACATATTTGATATACATAGTGCATATGATTTCTTACTTGAACAC	780		
QY 1307	ATCATGATATATGCAAAAATCTATGTAACGCCGCAACCGCTGCGGCTCTTCCAGGTGAC	1366		
DB 781	ATATATGATATATGCAAAAACCTGATGATGCGCATCGTTGTGACATTTTCCAGGTGAC	840		

QY 1367 CACAAGAAACAAGAGCTGTAACCTCGACCTGTTGACATTGGGGAGGAGAGAGGGGAG 1426  
 DB CATTAGAAACAAGAGATTATATTCAGACCTTTTGATTTGAGAGAGAGAGAGAGAGAGAG 900  
 QY 1427 CCCATCTTCAAGAAAGACAAGAGATCAGATTTTCCATTGAGAAAGGATGCTGTCTCA 1486  
 DB CCGTCTTCAAGAAAGACAAGAGATTAATTTTCAATTGAGAAAGATTTGCTGGCCAA 960  
 QY 1487 GTGGCAAGAAACGGGCAAGTCTTGAACATTTCCGATGCTTAGCGGAGCCCTGGCTTAA 1546  
 DB GTAGCAAGAAACGGGCAAGTCTTGAACATTTCCAGATGCTTAGCAGACCACGCTTAA 1020  
 QY 1547 AGGGAGTGAACCTGTACACGGGCTACACGAGAGAACTGTGTATGCGCAATAGAG 1606  
 DB AAGAAAGTATGATTTGACACAGGCTACACGCGGAACTCTGTGCAATGCCCATGTC 1080  
 QY 1607 AGCCGAGGAGCGGTGATTTGGCTGTGACAGATGTGAAACAAGTACAGCGGTAGCGCTTC 1666  
 DB AGCCGAGGAGCGGTGATTTGGCTGTGACAGATGTGAAACAAGTACAGCGGTAGCGCTTC 1140  
 QY 1667 TCBAAGACAGACGAGAAACAATTCAAGATGTTGCTGCTTCTGCGCACTGGCTTGCAC 1726  
 DB TCTAAACAGATGAAGAAACAATCTTCAAAATGTTGCGCTTCTTGTAGCTTACAC 1200  
 QY 1727 TGTGCTAATGATACACAGAGATCGGCACTGAGAAATGATCTACAGAGGTTACATAGAG 1786  
 DB TGTGCTAATGATATATATATGAAATTTGCTACAGATGCTACAGATGCTACAGATGCTT 1260  
 QY 1787 AAGCTTTCTTACACAGCATCTGCACTCTCGAGAGTGGCAAGGCTTACAGCGCTTCAAC 1846  
 DB AAGCTGCTTACATATGATGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1320  
 QY 1847 CTACACAGACGATCTGCGGAGACATCGAGCTATTCATTTGACATTTGCTTCTTGCAG 1906  
 DB CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
 QY 1907 AACATGTGGGCTGGGATCTTTGTCTACATGATCAATCGGCTGTTGGGACATCGCTTTT 1966  
 DB AACATGTGGGCTGGGATCTTTGTCTACATGATCAATCGGCTGTTGGGACATCGCTTTT 1440  
 QY 1967 GAATCTGAAAAATTTGCGGTTTATCATGTCTGTGAAAGAAACTATCGCGGCTTCT 2026  
 DB GAGCTTGAATAATTTGCTGTTTATATGCTGTGAAAGAAACTATCGCGGCTTCT 1500  
 QY 2027 TACCAAACTGAAAGCATGCACTGCTGCGGCACTGCTATGATGCTTCAAAAC 2086  
 DB TATCAAACTGAAAGCATGCTGCTGCACTGCTATGATGCTTCAAAAC 1560  
 QY 2087 AACATGTGGCTTCTTCAAGACCTCGAGGCAAAAGGCTGCTTATGCGGTCTGTGCTAT 2146  
 DB AATCAAGCTTCTTCAAGACCTCGAGGCAAAAGGCTGCTTATGCGGTCTGTGCTAT 1620  
 QY 2147 GACCTGACACAGAGGGCTTCACTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 2206  
 DB GACCTGACACAGAGGGCTTCACTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCTAAGCT 1680  
 QY 2207 GCGCTGTACTGCACTTCCAGATGAGCAACAATTCTCCAGACGCTGTCTCACTCTT 2266  
 DB GCTCTCTACTGCACTTCCAGATGAGCAACAATTCTCCAGACGCTGTCTCACTCTT 1740  
 QY 2267 CAGCTGAAAGGCAAAATTTCTTCTTCCACCTGAGAGTCAAGAGATGAGAGAGTGTCTG 2326  
 DB CAGCTGAAAGGCAAAATTTCTTCTTCCACCTGAGAGTCAAGAGATGAGAGAGTGTCTG 1800  
 QY 2327 GAGATCATCCGAAAGCATCATGCGCAAGCTCGCCCTATCTTGGGAAACGAGAG 2386  
 DB GAGATCATCCGAAAGCATCATGCGCAAGCTCGCCCTATCTTGGGAAACGAGAG 1860  
 QY 2387 CAGTTGAGAGATGTACCAAGCAGGGTGTCTGAACCTTCACAAACAGTCCCATGAGAC 2446  
 DB CAGTTGAGAGATGTACCAAGCAGGGTGTCTGAACCTTCACAAACAGTCCCATGAGAC 1920

QY 2447 CGTGTATCGGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2506  
 DB CGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980  
 QY 2507 GTTACAAATTTGACAGCGAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATG 2566  
 DB GTTACAAATTTGACAGCGAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATG 2040  
 QY 2567 AAGAGCTGGGATTCACCCCATTTCTGATGATGAGCAAGAGCAAGAGATGATGCTT 2626  
 DB AAGAAATTTGAGAAATGACCTTATGATGATGAGCAAGAGCAAGAGATGATGCTT 2100  
 QY 2627 CAGGCGAGCTCGATTTCAACAATGCTGAGCATTTCCCTGATATACACTTGAAGAG 2686  
 DB CAGGCGAGCTCGATTTCAACAATGCTGAGCATTTCCCTGATATACACTTGAAGAG 2160  
 QY 2687 ATCTCCCAACCAAGACCTTCTGTAAGGCTGAGGAGTAACCTGAATGATGAGAG 2746  
 DB ATCTCCCTCCCAAGAGCTTCTTCTGAAGATGCAAGAGATGATGATGATGATGATG 2220  
 QY 2747 AAGTATTTCCGAGGAGAGAGACAGCAATGTGATTTGAGGCCCGAGGCCGCGC 2801  
 DB AAGTATTTCCGAGGAGAGAGACAGCAATGTGATTTGAGGCCCGAGGCCGCGC 2275

## RESULT 11

US-08-951-648-38  
 ; Sequence 38, Application US/08951648  
 ; Patent No. 5932465  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loughney, Kate  
 ; TITLE OF INVENTION: Phosphodiesterase 8  
 ; NUMBER OF SEQUENCES: 38  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 233 South Wacker, Sears Tower Suite 6300  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: US  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/951,648  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Williams Jr., Joseph A.  
 ; REGISTRATION NUMBER: 38,659  
 ; REFERENCE/DOCKET NUMBER: 27866/34038  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312-474-6300  
 ; TELEFAX: 312-474-0448  
 ; INFORMATION FOR SEQ ID NO: 38:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 477 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: CDNA  
 ; US-08-951-648-38

## Query Match 13.0%; Score 469.2; DB 2; Length 477;

Best Local Similarity 99.4%; Pred. No. 5e-99;  
 Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAGCCGAGGATTTGACATGTAATCTTTGAGAGTGCATTAATTAAGCTGTGTGT 864  
 DB 4 CCAAAAGCCGAGGATTTGACATGTAATCTTTGAGAGTGCATTAATTAAGCTGTGTGT 63

QY 865 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGCAAGGCCCATCAG 924  
DB 64 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGCGGGGCCCATCAG 123  
QY 925 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 984  
DB 124 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 183  
QY 985 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 1044  
DB 184 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 243  
QY 1045 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 1104  
DB 244 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 303  
QY 1105 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 1164  
DB 304 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 363  
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 1224  
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 423  
QY 1225 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 1278  
DB 424 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 477

RESULT 12  
US-09-174-437-38  
; Sequence 38, Application US/09174437A  
; Patent No. 6133007  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/174,437A  
; EARLIER FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 08/951,648  
; EARLIER FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 477  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-174-437-38

Query Match 13.0%; Score 469.2; DB 3; Length 477;  
Best Local Similarity 99.4%; Pred. No. 5e-99;  
Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAAGCCGAGCGAATTTGCACTGTACTTCTTGGAGAGTGCAATAATAGCTGTGTGT 864  
DB 4 CCAAAAAGCCGAGCGAATTTGCACTGTACTTCTTGGAGAGTGCAATAATAGCTGTGTGT 63  
QY 865 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGAGGGGCCCATCAC 924  
DB 64 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGAGGGGCCCATCAC 123  
QY 925 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 984  
DB 124 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 183  
QY 985 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 1044  
DB 184 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 243  
QY 1045 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 1104  
DB 244 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 303

QY 1105 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 1164  
DB 304 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 363  
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 1224  
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 423  
QY 1225 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 1278  
DB 424 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 477

RESULT 13  
US-09-686-055A-38  
; Sequence 38, Application US/09686055A  
; Patent No. 6566087  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/686,055A  
; EARLIER FILING DATE: 2000-10-11  
; EARLIER APPLICATION NUMBER: 08/951,648  
; EARLIER FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38  
; LENGTH: 477  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-686-055A-38

Query Match 13.0%; Score 469.2; DB 3; Length 477;  
Best Local Similarity 99.4%; Pred. No. 5e-99;  
Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAAGCCGAGCGAATTTGCACTGTACTTCTTGGAGAGTGCAATAATAGCTGTGTGT 864  
DB 4 CCAAAAAGCCGAGCGAATTTGCACTGTACTTCTTGGAGAGTGCAATAATAGCTGTGTGT 63  
QY 865 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGAGGGGCCCATCAC 924  
DB 64 GTTCATACCACTGGGATGAGAGAGCCCAACCCGGCTCATCTCTGAGGGGCCCATCAC 123  
QY 925 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 984  
DB 124 CCAAGGATACCACTCTCTGCTCCCTACGTCGCGCAAGCTATAGAGAGAGCTTTGGGTAGAGGA 183  
QY 985 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 1044  
DB 184 TATCTTGGGGATGAGAGAGATTTCTCTGAGGATCTGCGCTGGAATCAGAAACCCGCATCCA 243  
QY 1045 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 1104  
DB 244 GTCTGTTCTTGGCTTGGCCCATGTCACCTGCACTTGGAGACTTGATTTGGCATCTTTGAAC 303  
QY 1105 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 1164  
DB 304 GTACAGGCACTGGGGAGAAAGAGCCCTTGGCTCAGCCATCAGAGAGTTGGCAACAGCCAA 363  
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 1224  
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGAGGTCTCGCAAAACA 423  
QY 1225 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 1278  
DB 424 GACCGAAGTGAATGACTTCTCTACTGACGTATCAAGACATCTTTGATTAACAT 477

RESULT 14  
US-08-951-648-33  
; Sequence 33, Application US/08951648

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; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker, Sears Tower Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-951-648-33

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Query Match          9.3%; Score 333.8; DB 2; Length 404;
Best Local Similarity 92.6%; Pred. No. 1.2e-67;
Matches 373; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 1298 CTTGAACATCATATATATGCAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTC 1357
DB 1 CTTGAACATCATATATATGCAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTC 60

QY 1358 CAGGTGACCAACAAGAGAGCTGTACTCGGACCTGTTGAACATTGGGAGAGAAAG 1417
DB 61 CAGGTGACCAACAAGAGAGCTGTACTCGGACCTGTTGAACATTGGGAGAGAAAG 120

QY 1418 GAGGGGAAGCCCATCTTCAAGAAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATT 1477
DB 121 GAGGGGAAGCCCGTTTCAAGAAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATT 180

QY 1478 GCTGTCAGAGTGGCAAGAACAGCGCAAGTCTTGAACATTCGCCATGCCACGACCT 1537
DB 181 GCTGTCAGAGTGGCAAGAACAGCGCAAGTCTTGAACATTCGCCATGCCACGACCT 240

QY 1538 CGCTTTAACAAGAGGTGACCTGTACACAGGCTACACCAAGAGAACTTCTGTGTATG 1597
DB 241 CGCTTTAACAAGAGGTGACCTGTACACAGGCTACACCAAGAGAACTTCTGTGTATG 300

QY 1598 CCCATAGTAGGCGGAGCGGACGCTGATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 1656
DB 301 CCCATAGTAGGCGGAGCGGACGCTGATTGGCGTGTGACAGATGGTTTAAACAAGATCAGCGG 360

QY 1657 TAGCGCTTCTCCAGAACAAGAGAACTTCAAGATGTTT 1699
DB 361 CA--GGCCTTTCAGAAGCGAGATGAGAACTTCAAGATGTTT 401

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RESULT 15  
US-09-174-437-33  
; Sequence 33, Application US/09174437A

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; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 33
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-174-437-33

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Query Match          9.3%; Score 333.8; DB 3; Length 404;
Best Local Similarity 92.6%; Pred. No. 1.2e-67;
Matches 373; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 1298 CTTGAACATCATATATATGCAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTC 1357
DB 1 CTTGAACATCATATATATGCAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTC 60

QY 1358 CAGGTGACCAACAAGAGAGCTGTACTCGGACCTGTTGAACATTGGGAGAGAAAG 1417
DB 61 CAGGTGACCAACAAGAGAGCTGTACTCGGACCTGTTGAACATTGGGAGAGAAAG 120

QY 1418 GAGGGGAAGCCCATCTTCAAGAAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATT 1477
DB 121 GAGGGGAAGCCCGTTTCAAGAAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATT 180

QY 1478 GCTGTCAGAGTGGCAAGAACAGCGCAAGTCTTGAACATTCGCCATGCCACGACCT 1537
DB 181 GCTGTCAGAGTGGCAAGAACAGCGCAAGTCTTGAACATTCGCCATGCCACGACCT 240

QY 1538 CGCTTTAACAAGAGGTGACCTGTACACAGGCTACACCAAGAGAACTTCTGTGTATG 1597
DB 241 CGCTTTAACAAGAGGTGACCTGTACACAGGCTACACCAAGAGAACTTCTGTGTATG 300

QY 1598 CCCATAGTAGGCGGAGCGGACGCTGATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 1656
DB 301 CCCATAGTAGGCGGAGCGGACGCTGATTGGCGTGTGACAGATGGTTTAAACAAGATCAGCGG 360

QY 1657 TAGCGCTTCTCCAGAACAAGAGAACTTCAAGATGTTT 1699
DB 361 CA--GGCCTTTCAGAAGCGAGATGAGAACTTCAAGATGTTT 401

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OW nucleic - nucleic search, using BW model

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Perfect score: 3606  
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

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10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3606	100.0	3606	3	US-09-321-801-14 Sequence 14, Appl
2	3606	100.0	3606	7	US-10-618-252-14 Sequence 14, Appl
3	3064	85.0	7618	7	US-10-659-770-12 Sequence 12, Appl
4	3050.4	84.6	7581	7	US-10-659-770-11 Sequence 11, Appl
5	2610.6	72.4	3219	5	US-10-202-107-11 Sequence 11, Appl
6	2610.6	72.4	3219	8	US-10-887-276-1 Sequence 1, Appl
7	1871.8	51.9	4389	6	US-10-440-998-3 Sequence 1, Appl
8	1858.4	51.5	2554	3	US-09-321-801-1 Sequence 1, Appl
9	1858.4	51.5	2554	7	US-10-618-252-1 Sequence 3, Appl
10	1790.2	49.6	2798	3	US-09-321-801-3 Sequence 3, Appl
11	1790.2	49.6	2798	7	US-10-618-252-3 Sequence 5, Appl
12	1787.4	49.6	3195	6	US-10-440-998-5 Sequence 5, Appl
13	1787.4	49.6	4381	3	US-09-420-190-2 Sequence 2, Appl
14	1787.4	49.6	4381	6	US-10-458-839-2 Sequence 2, Appl
15	1785	49.5	2298	6	US-10-440-998-1 Sequence 1, Appl
16	900.2	25.0	1068	3	US-09-321-801-12 Sequence 12, Appl
17	900.2	25.0	1068	7	US-10-618-252-12 Sequence 12, Appl
18	485.2	13.5	539	3	US-09-321-801-18 Sequence 18, Appl
19	485.2	13.5	539	7	US-10-618-252-18 Sequence 18, Appl
20	484.2	13.4	4446	9	US-10-450-763-23296 Sequence 23296, A
21	469.2	13.0	477	6	US-10-440-998-38 Sequence 38, Appl
22	441.4	12.2	487	3	US-09-321-801-16 Sequence 16, Appl
23	441.4	12.2	487	7	US-10-618-252-16 Sequence 16, Appl

24	333.8	9.3	404	6	US-10-440-998-33 Sequence 33, Appl
25	272.6	7.6	458	6	US-10-440-998-7 Sequence 7, Appl
26	216.6	6.0	3489	6	US-10-168-402-5 Sequence 5, Appl
27	216.6	6.0	4167	6	US-10-168-402-5 Sequence 38, Appl
28	215.4	6.0	3855	10	US-11-097-143-42398 Sequence 42398, A
29	209.6	5.8	3044	3	US-09-883-825-44 Sequence 44, Appl
30	209.6	5.8	3044	7	US-10-697-894-44 Sequence 44, Appl
31	209.6	5.8	4145	7	US-10-236-417-77 Sequence 77, Appl
32	209.6	5.8	4171	5	US-10-094-989-1 Sequence 1, Appl
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36	209.6	5.8	4240	8	US-10-686-282-6 Sequence 2038, Ap
37	209.6	5.8	4240	9	US-10-843-641A-2038 Sequence 6, Appl
38	209.6	5.8	4240	9	US-10-686-349-6 Sequence 1917, Ap
39	209.6	5.8	4240	9	US-10-756-149-1917 Sequence 485, App
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41	201.6	5.6	1784	5	US-10-094-168B-2 Sequence 6, Appl
42	201.6	5.6	1784	7	US-10-746-197-6 Sequence 2, Appl
43	201.6	5.6	2078	7	US-10-746-197-2 Sequence 8, Appl
44	201.6	5.6	2502	3	US-09-891-216-8 Sequence 9, Appl
45	201.6	5.6	2889	3	US-09-891-216-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-09-321-801-14  
Sequence 14, Application US/09321801  
Patent No. US20020115176A1  
GENERAL INFORMATION:  
APPLICANT: Lanfear, Jeremy  
APPLICANT: Robas, Nicola M.  
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
FILE REFERENCE: PC9477A  
CURRENT APPLICATION NUMBER: US/09/321, 801  
EARLIER FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: 9626777.6  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: 9623882.7  
EARLIER FILING DATE: 1998-10-30  
EARLIER APPLICATION NUMBER: 9811500.9  
EARLIER FILING DATE: 1998-05-28  
EARLIER APPLICATION NUMBER: 9908247.1  
EARLIER FILING DATE: 1998-04-09  
EARLIER APPLICATION NUMBER: 9910801.1  
EARLIER FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 3606  
TYPE: DNA  
ORGANISM: Mouse  
US-09-321-801-14  
Query Match 100.0%; Score 3606; DB 3; Length 3606;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3606; Mismatches 0; Indels 0; Gaps 0;  
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 RESULT 2  
 US-10-618-252-14  
 ; Sequence 14, Application US/10618252  
 ; Publication No. US20040018542A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lanfear, Jeremy  
 ; APPLICANT: Rodas, Nicola M.  
 ; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
 ; FILE REFERENCE: PC9477B  
 ; CURRENT APPLICATION NUMBER: US/10/618,252  
 ; PRIOR FILING DATE: 2003-07-11  
 ; PRIOR APPLICATION NUMBER: 9826777.6  
 ; PRIOR FILING DATE: 1998-12-04  
 ; PRIOR APPLICATION NUMBER: 9823882.7  
 ; PRIOR FILING DATE: 1998-10-30  
 ; PRIOR APPLICATION NUMBER: 9811500.9  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 9908247.1  
 ; PRIOR FILING DATE: 1999-04-09  
 ; PRIOR APPLICATION NUMBER: 9910801.1  
 ; PRIOR FILING DATE: 1999-05-10  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 14  
 ; LENGTH: 3606  
 ; TYPE: DNA  
 ; ORGANISM: Mouse  
 US-10-618-252-14  
 Query Match 100.0%; Score 3606; DB 7; Length 3606;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
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1261 GACATATCTTGTAAATATGTTGCCATAGACTCTCTTACTTGAACATCATGATATATGC 1320  
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1321 AAAAAATCTAGTAAACGCGACCGCTGCGCTTCCAGGTGACCAAAAGCAAGGA 1380  
1381 GGTGTACTGAGACTGTTTGAATTTGGGAGAGAAAGAGGAGCCATCTTCAAGA 1440  
1381 GGTGTACTGAGACTGTTTGAATTTGGGAGAGAAAGAGGAGCCATCTTCAAGA 1440  
1441 GACCAAGAGATCAATTTTCAATTTGAGAAAGGATTTGTGTCAAGTGGCAAGACAG 1500  
1441 GACCAAGAGATCAATTTTCAATTTGAGAAAGGATTTGTGTCAAGTGGCAAGACAG 1500

1501 CGAAGCTTTGAACATTTCCGATGCTTACGCGAGACCTCGCTTTAAACAGGAGGTGACCT 1560  
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1741 CCACAGAGATCCGCACTGAGAAATGATCTACAGGGTACATGAGAGCTTCTTACCA 1800  
1741 CCACAGAGATCCGCACTGAGAAATGATCTACAGGGTACATGAGAGCTTCTTACCA 1800  
1801 CAGCATCTGCACTCTCCGAGAGTGGCAAGGCTCATGGCTTCAACCTACAGACAGCAT 1860  
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1921 GATCTTGTCTTACATGATCATCGGTCTGTGGAGCATCTGTCTTGAACCTTGAATAAT 1980  
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2041 GCATCAGTACAGGGGCACTGATGTATGCACTTCAAAACAATGAGCTCTT 2100  
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2401 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460  
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DB 2641 ATTCAATATGCTGTGGCCATTCCTGCTATATCAACCTTGAAGCAGATCTCCACCCAC 2700  
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DB 2701 AGAGCTTCTGTGAAGGCTGTGAGGATTAACCTCAATCAGTGGAGAGATTAATTCGCGG 2760  
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DB 2761 GGAAGAGACAGAAATGTGATTTCAAGGCCAGGCCGCGGCTTAGAAGACACCTGA 2820  
QY 2821 GAAAGCTGAACGTGAAGGTTGAAGACTGATCTGAAGTGAAGTCTGATCTGCGCAGCA 2880  
DB 2821 GAAAGCTGAACGTGAAGGTTGAAGACTGATCTGAAGTGAAGTCTGATCTGCGCAGCA 2880  
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DB 2881 ACCGACTCAACCTGCTTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 2940  
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DB 2941 GTCAAGAGTACCTGTGCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3000  
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DB 3001 CTGCGACATGAGCAACCCAGGCTGCGGCTGTTGAGAGTCTGAGTCTGAGTCTGAGTCT 3060  
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DB 3121 ACCACAGAGAGGTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3180  
QY 3181 GTGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240  
DB 3181 GTGCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3240  
QY 3241 GTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300  
DB 3241 GTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300  
QY 3301 GGTCAAGTCCACAGGTTGACAGAGAAATCCAACTGTTGATTAAGGTGCACTACAGGTA 3360  
DB 3301 GGTCAAGTCCACAGGTTGACAGAGAAATCCAACTGTTGATTAAGGTGCACTACAGGTA 3360  
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DB 3361 TGTCTTTTCAAGTATCTGAGGAGGACATAGGTGATGCTGCTCACTCAGAGAGAGATTA 3420  
QY 3421 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480  
DB 3421 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480  
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DB 3601 AAAAAA 3606

RESULT 3

US-10-659-770-12  
Sequence 12, Application US/10659770  
Publication No. US20040152106A1  
GENERAL INFORMATION:  
APPLICANT: ROBERTSON, Harold  
APPLICANT: DENOVAN-WRIGHT, Eileen  
APPLICANT: NOVANEURON, INC.  
TITLE OF INVENTION: GENE NECESSARY FOR STRIATAL FUNCTION,  
TITLE OF INVENTION: USES THEREOF, AND  
TITLE OF INVENTION: COMPOUNDS FOR MODULATING SAME  
FILE REFERENCE: 2817/102  
CURRENT APPLICATION NUMBER: US/10/659,770  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 09/680,208  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 60/217,765  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: 60/158,043  
PRIOR FILING DATE: 1999-10-07  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FaSTSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 7618  
TYPE: DNA  
ORGANISM: mouse  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (7075)...(7076)  
OTHER INFORMATION: a or g or c or t/u, unknown or other  
US-10-659-770-12

Query Match 85.0%; Score 3064; DB 7; Length 7618;  
Best Local Similarity 99.6%; Pred. No. 0; Mismatches 11; Indels 0; Gaps 0;  
Matches 3070; Conservative 1;

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DB 273 GTTTGACGATGAAGAGGCTATCTTCTCTCCATCCCAAGTATTAGATGAAT 584  
QY 585 TTGTTTCTGAAGAGTGTAGTGAAGAGCTGTGAGAAAGTGGCTGAAGAGAAACCAACA 644  
DB 333 TTGTTTCTGAAGAGTGTAGTGAAGAGCTGTGAGAAAGTGGCTGAAGAGAAACCAACA 644  
QY 645 AAGCAAAATGAACATCTTCCCAAGAGTCAAGAGGATTAAGATTAAGATTAAGATTA 704  
DB 393 AAGCAAAATGAACATCTTCCCAAGAGTCAAGAGGATTAAGATTAAGATTAAGATTA 704  
QY 705 GAGTGTGACGAGTGAACAGTACATAGAGAGGCTGACAGAGGAGGAGGAGGAGGAGG 764  
DB 453 GAGTGTGACGAGTGAACAGTACATAGAGAGGCTGACAGAGGAGGAGGAGGAGGAGG 764  
QY 765 ACCTGCTCTTATGAGCTCAGCAGCATCATCAGATTAAGATTAAGATTAAGATTAAG 824  
DB 513 ACCTGCTCTTATGAGCTCAGCAGCATCATCAGATTAAGATTAAGATTAAGATTAAG 824  
QY 825 CACTGATCTTCTTGAAGAGTGAATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 884  
DB 573 CACTGATCTTCTTGAAGAGTGAATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 884  
QY 885 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 944  
DB 633 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 944  
QY 945 CTTACGTGAGCAAGTGAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1004  
DB 693 CTTACGTGAGCAAGTGAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1004  
QY 1005 TTCTTGAAGTACTGCTGTGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1064  
DB 753 TTCTTGAAGTACTGCTGTGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1064  
QY 1065 TTGTCATGCTGATTTGAGAGCTTGAATGCACTTTGAACGTGACAGGCACTGGGGCAAG 1124  
DB 1065 TTGTCATGCTGATTTGAGAGCTTGAATGCACTTTGAACGTGACAGGCACTGGGGCAAG 1124



Db 813 TTGTGACTGCGCATTTGAGACCTTATTTGGACCTTTGAACCTGTACAGGCACTGGGGCAAG 872  
Qy 1125 AGGCGTTGCGCTCAGCCATCGAGGAGTTTGGCAAGCCAACTGTGCTGGGCTTCGGTAG 1184  
Db 873 AGGCGTTGCGCTCAGCCATCGAGGAGTTTGGCAAGCCAACTGTGCTGGGCTTCGGTAG 932  
Qy 1185 CAATACACGAGGTGAGGTGTGTAGAGGTCTCGCCAAACAGACCGAACCTGAATGACTTCC 1244  
Db 933 CAATACACGAGGTGAGGTGTGTAGAGGTCTCGCCAAACAGACCGAACCTGAATGACTTCC 992  
Qy 1245 TACTGAGGTATCAAAAGACATCTTTGATTAACATAGTTGCCATPAGACTCTTACTTTGAAC 1304  
Db 993 TACTGAGGTATCAAAAGACATCTTTGATTAACATAGTTGCCATPAGACTCTTACTTTGAAC 1052  
Qy 1305 ACATCATGATATATGCAAAAATCTAGTGAAGCGGACCGCTGGCGCTTCCAGGTGG 1364  
Db 1053 ACATCATGATATATGCAAAAATCTAGTGAAGCGGACCGCTGGCGCTTCCAGGTGG 1112  
Qy 1365 ACCACAAGAACAAAGAGCTGTACTCGGACCTGTTTGACA TTGGGGAGAGAAAGAGGGA 1424  
Db 1113 ACCACAAGAACAAAGAGCTGTACTCGGACCTGTTTGACA TTGGGGAGAGAAAGAGGGA 1172  
Qy 1425 AGCCCATCTTCAAGAAACCAAGAGATCAGATTTTCCATTGAAGAAAGGGA TTGCTGTGC 1484  
Db 1173 AGCCCATCTTCAAGAAACCAAGAGATCAGATTTTCCATTGAAGAAAGGGA TTGCTGTGC 1232  
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Db 1233 AAGTGGCAAGAACAGGCGCAAGCTTGAACATTCGCCGATGCCGACCTCGCTTTA 1292  
Qy 1545 AAGTGGAGGTGAGCTGTACACAGGCTACACCAAGAACAACTTGTGTATGCCCATAG 1604  
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Qy 1605 TGAAGCCGAGCGCTGATTTGGCTGTGTGCAAGTGTGAACAAAGATCAGCGGTAGCGCT 1664  
Db 1353 TGAAGCCGAGCGCTGATTTGGCTGTGTGCAAGTGTGAACAAAGATCAGCGGTAGCGCT 1412  
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Qy 1725 ACTGTGCTAACTGTACCAAGAGATCCGCACTCAGAAATGCACTTCAAGGGTTAACATAG 1784  
Db 1473 ACTGTGCTAACTGTACCAAGAGATCCGCACTCAGAAATGCACTTCAAGGGTTAACATAG 1532  
Qy 1785 AGAAGCTTTCCTACCAAGCATCTGCACTCCGAGAGAGTGGCAAGGCTCATGCGCTTCA 1844  
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Db 1593 ACCTTACGAGAGCATCTGCGGGGACATCGAGCTATTCACCTTTGACATTTGGTCTTTTGC 1652  
Qy 1905 AGAATGATGGCTGGGATCTTTGTCTACATGATCCATCGGTCTTGGGGACATCTGTT 1964  
Db 1653 AGAATGATGGCTGGGATCTTTGTCTACATGATCCATCGGTCTTGGGGACATCTGTT 1712  
Qy 1965 TTGAACCTGAAAATTTGTGCGCTTTTATCATGTCTGTGAAGAAAGACTATCGGCGGGTTC 2024  
Db 1713 TTGAACCTGAAAATTTGTGCGCTTTTATCATGTCTGTGAAGAAAGACTATCGGCGGGTTC 1772  
Qy 2025 CTTTACCAACATGGAAGCATGCAAGTCAAGGTGGCACTGCAATGTATGCAATCTTCAAA 2084  
Db 1773 CTTTACCAACATGGAAGCATGCAAGTCAAGGTGGCACTGCAATGTATGCAATCTTCAAA 1832  
Qy 2085 ACAACATGGGCTCTTCAACAGACTCGAGCGCAAAAGGCTGCTAAATTGGGTGTCTGTGC 2144  
Db 1833 ACAACATGGGCTCTTCAACAGACTCGAGCGCAAAAGGCTGCTAAATTGGGTGTCTGTGC 1892  
Qy 2145 ATGACCTGGACCAAGGGCTTCAAGTAAACAGCTACCTGCAAGAGTTTCAGACACCCCTGG 2204  
Db 1893 ATGACCTGGACCAAGGGCTTCAAGTAAACAGCTACCTGCAAGAGTTTCAGACACCCCTGG 1952

Qy 2205 CGGCGCTGTACTCCACCTCCACATGAGCAACCACTTCTCCGACGAGTGTCCATCC 2264  
Db 1953 CGGCGCTGTACTCCACCTCCACATGAGCAACCACTTCTCCGACGAGTGTCCATCC 2012  
Qy 2265 TTCAAGTGAAGGGCAAAATCTTCTCCACCTCGAGTCCAGAGGATACAGACAGTGTGC 2324  
Db 2013 TTCAAGTGAAGGGCAAAATCTTCTCCACCTCGAGTCCAGAGGATACAGACAGTGTGC 2072  
Qy 2325 TGGAGATCATCGGAAGCCATCATCGGCACCGACCTGCGCTTATCTTTGGGAAACAGGA 2384  
Db 2073 TGGAGATCATCGGAAGCCATCATCGGCACCGACCTGCGCTTATCTTTGGGAAACAGGA 2132  
Qy 2385 AGCAGTTGAGAGAGATGTACAGACAGGGGTGCTGAACCTCCACAAACAGTCCCATCGAG 2444  
Db 2133 AGCAGTTGAGAGAGATGTACAGACAGGGGTGCTGAACCTCCACAAACAGTCCCATCGAG 2192  
Qy 2445 ACCGTGTATCGGCTTGAATGATGACTGCTGTGATCTTTGCTCTGTGACCAAACTATGGC 2504  
Db 2193 ACCGTGTATCGGCTTGAATGATGACTGCTGTGATCTTTGCTCTGTGACCAAACTATGGC 2252  
Qy 2505 CAGTTACAAAATTTGACAGCGAATGATATATATGCAAGATTTCTGGGCTGAGGGGTATGGA 2564  
Db 2253 CAGTTACAAAATTTGACAGCGAATGATATATATGCAAGATTTCTGGGCTGAGGGGTATGGA 2312  
Qy 2565 TGAAGAAGCTGGGCAATACAGCCCATTTCTATGATGACAGAGACAAAGCAGATGAAGTCC 2624  
Db 2313 TGAAGAAGCTGGGCAATACAGCCCATTTCTATGATGACAGAGACAAAGCAGATGAAGTCC 2372  
Qy 2625 CTCAAGGGCAGCTCGGATTTTCAAACTGTGTGGCCATTCCTGTCTATACACTTTGACGC 2684  
Db 2373 CTCAAGGGCAGCTCGGATTTTCAAACTGTGTGGCCATTCCTGTGTATACCACTTTGACGC 2432  
Qy 2685 AGATCTCCACCAACAGAGCTGTGTGAAGGCTGTGAAGGCTGTGAAGGATTAACCTCAATCAGTGG 2744  
Db 2433 AGATCTCCACCAACAGAGCTGTGTGAAGGCTGTGAAGGCTGTGAAGGATTAACCTCAATCAGTGG 2492  
Qy 2745 AGAAGTAAATTCGCGGGAGAAAGACAGCAATGTGATTTCAAGGCCAGGCCGCGGCTTA 2804  
Db 2493 AGAAGTAAATTCGCGGGAGAAAGACAGCAATGTGATTTCAAGGCCAGGCCGCGGCTTA 2552  
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Db 2553 GCAAGAGCAACCTGAGAGGCTTGAAGCTTGAAGCTGAACTGATCTGAAAGTACGTCC 2612  
Qy 2865 TGAATGTGCGCCAGGAACCGACTCAACCTGCTTCTGTGACCTTCTTTTGTGTTTCAA 2924  
Db 2613 TGAATGTGCGCCAGGAACCGACTCAACCTGCTTCTGTGACCTTCTTTTGTGTTTCAA 2672  
Qy 2925 GGGGTGAAGAACCCCTGTCAAGAGGTACCGTCCGATATCCATGTGAACAGACGACTCC 2984  
Db 2673 GGGGTGAAGAACCCCTGTCAAGAGGTACCGTCCGATATCCATGTGAACAGACGACTCC 2732  
Qy 2985 TGTTCGCGCAACAACCTCGAAGTGAAGAACCCAGGCTGTGCGGTTCAGAGCTGCG 3044  
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Qy 3045 CTAATCTCGGTGCTCACTGACCTTCCGAATGTATTTGCTCCAGGCGAAGCATGCACTG 3104  
Db 2793 CTAATCTCGGTGCTCACTGACCTTCCGAATGTATTTGCTCCAGGCGAAGCATGCACTG 2852  
Qy 3105 TCTGGAAGGGGCAAGACCAAGAGAGGTTCTTGGCTGCAATCCCTCCATGAGGGGTGCG 3164  
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Qy 3165 CCAAGTTCCCTGTGCTGTGCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 3224  
Db 2913 CCAAGTTCCCTGTGCTGTGCAATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2972  
Qy 3225 CGCCCTTGTGTGAAGTTTACATGTGACCTTCTTATAGTTTAACTGAGTTTGTGGCTGG 3284  
Db 2973 CGCCCTTGTGTGAAGTTTACATGTGACCTTCTTATAGTTTAACTGAGTTTGTGGCTGG 3032



[illegible][illegible]

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1233 AAGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCCGATGCTTACGGGGAACCTCGCTTAA 1292  
1545 ACAAGGAGGTGGAACCTGTACACAGGCTTACACAGAGGAACATTTGTGTATGCTCCATAG 1604  
1293 ACAAGGAGGTGGAACCTGTACACAGGCTTACACAGAGGAACATTTGTGTATGCTCCATAG 1352  
1605 TGAAGCGAGGCAAGCGATTTGGCGGTGTGACATGCTGTAACAAGATCAGCGGTAGCGCT 1664  
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1413 TCTCCAAAGCAGACAGAGAACAACTTCAAGATGTTTGTCTGTCTGTGCGCACTGCGCTTGC 1472  
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1473 ACTGTGCTAACATGTACCAAGAGATCGCCACTCAGAGATGCAATCTACAGGGTTAACATGG 1532  
1785 AAGAGCTTTCCTACCAAGACATCTGCACTCCGAGAGATGGCAAGGCTTCATGCGCTTCA 1844  
1533 AAGAGCTTTCCTACCAAGACATCTGCACTCCGAGAGATGGCAAGGCTTCATGCGCTTCA 1592  
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1773 CTTTACCAACATGGAAGCATGAGATCGAGTGCACACTGCAATGTATGCAATCTTCAAA 1832  
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1833 ACAACATATGAGCTCTTACACAGACCTTGAGCGCAAGGCTTGCTAAATGCGTGTCTGTGC 1892  
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2205 CGGCGCTGTACTCACCCTCCACATGGAAGCAACCACTTCTCCGAGAGGTGCATATCC 2264  
1953 CGGCGCTGTACTCACCCTCCACATGGAAGCAACCACTTCTCCGAGAGGTGCATATCC 2012  
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2745 AAGAGTAATTCGCGGGGAGAGACAGCAATGTGGAATTTCAAGGCCAGGCCCGCGCTTA 2804  
2493 AAGAGTAATTCGCGGGGAGAGACAGCAATGTGGAATTTCAAGGCCAGGCCCGCGCTTA 2552  
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2613 TGAATGTGCGCCAGCAACCGACTCAACCTGCTGTGTAAGCTTGCCTTTTGTGTTTCAA 2672  
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RESULT 5  
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; Sequence 1, Application US/10202107  
; Publication No. US20030096323A1  
GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: James, Larry C.  
; APPLICANT: Leibel, Lorraine A.  
; APPLICANT: Menikoff, Frank S.  
; APPLICANT: Strick, Christine A.  
; TITLE OF INVENTION: PD510 CELL-BASED ASSAY AND SEQUENCES  
; FILE REFERENCE: PC21111ANIS  
; CURRENT APPLICATION NUMBER: US/10/202,107  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/308,978  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO: 1  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Rattus sp.  
US-10-202-107-1

Query Match 72.4%; Score 2610.6; DB 5; Length 3219;  
Best Local Similarity 91.9%; Pred. No. 0;  
Matches 2844; Conservative 0; Mismatches 214; Indels 35; Gaps 7;

525 GTTTGACGATGAAAGGTGAGAGGCTATCTTCTCCATCCCGGTTATTGAGAT 584  
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DB 2342 TCAGAGGAGAGAGACTGCACACTGATTTCAATCCCATCCGTGGCTC 2388

RESULT 8
US-09-321-801-1
; Sequence 1, Application US/09321801
; Patent No. US2002015176A1
; GENERAL INFORMATION:
; APPLICANT: lanfeart, Jeremy
; APPLICANT: Robae, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321,801
; EARLIER FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; EARLIER FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Human
US-09-321-801-1

Query Match 51.5%; Score 1858.4; DB 3; Length 2554;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 9908247.1  
 ; PRIOR FILING DATE: 1999-04-09  
 ; PRIOR APPLICATION NUMBER: 9910801.1  
 ; PRIOR FILING DATE: 1999-05-10  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: Patent Ver. 3.2  
 ; SEQ ID NO: 1  
 ; LENGTH: 2554  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 us-10-618-252-1  
  
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 Best Local Similarity 86.8%; Pred. No. 0;  
 Matches 2045; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

QY 446 TTCGGCTCCGACATGGAAGATGACCCCTTAAACAATGCGAGTTGCTTCGGAAGGCTGACC 505  
 DB 1 TTCGGCTCCGACATGGAAGATGACCTTCTAATATGCGAGCTGCTTCGGAAGGCTGACC 60  
 QY 506 GAGTGTCTCCAGAGCCGAGTTTGAAGGATGAAAGTGAAGGCTATCTTCTCCAT 565  
 DB 61 GAGTGTCTCCAGAGCCGAGTTTGAAGGATGAAAGTGAAGGCTATCTTCTCCAT 120  
 QY 566 CCCAGGATTTAGATGAAATTTGTTTCTGAAGTGTAGTGCAGAGACTGTGAAAAGTGG 625  
 DB 121 CCCAGGATTTAGATGAAATTTGTTTCTGAAGTGTAGTGCAGAGACTGTGAAAAGTGG 180  
 QY 626 CTGAAGAGAAAACCAACAAAGGAAAGATGAAACATTTCCCAAGGAAGTCAAGCAGTAC 685  
 DB 181 CTGAAGAGAAAACCAACAAAGTGAAGATGATCAGCTCTTAAGAAAGTCAAGCAGTAC 240  
 QY 686 CAGGATACGAATATGAGAGGAGTGTGTACAGCTGACGATACATAGACAGCCCTG 745  
 DB 241 CAGGATACGAATATGAGAGGAGTGTGTATATGAATTAACAGCTATATAGAACACGGTTG 300  
 QY 746 GACACGGGCGGGGCAACCACTGTCTCTATGAGCTCAGACGATCATCAGATATGCC 805  
 DB 301 GACACGGGCGGGGCAACCACTGTCTCTATGAGCTCAGACGATCATTAATAATATGCC 360  
 QY 806 ACAAAGCCGAGCGGATTTGCACTGTACTTCTTGGAGAGTGCATAATAGCCCTGTGTG 865  
 DB 361 ACAAAGCCGAGCGGATTTGCACTGTATTTCTTGGAGAGTGCATAATAGCCCTGTGTG 420  
 QY 866 TTCTATACACCCCGGATGGAAGAAAGCAACCCCGCTCATCCCTGAGGGGCCATACCC 925  
 DB 421 TTCTATACACCCCGGATGGAAGAAAGCAACCCCGCTCATCCCTGAGGGGCCATACCT 480  
 QY 926 CAGGATACCACTCTCTGCTACGTGGCCAGTCTTAAGAAAGCTTTGTGTAGAGAT 985  
 DB 481 CAGGATACCACTCTCTGCTTATGTGGCCAGTCTTAAGAAAGCTTTGTGTAGAGAT 540  
 QY 986 ATCTTTGGGATGAGCGATTTCTCGAGGTACTGGCTGGAATCAGAACCCGATCCAG 1045  
 DB 541 ATCTTTGGGATGAGCGATTTCTCAAGAGGTACTGGAATCAGAGGACTCGATATCCAG 600  
 QY 1046 TCTGTTCTTTGCTTGGCCATTTGCACTGCGCATTTGGAGACTTTGATTTGGCATCTTGAAC 1105  
 DB 601 TCTGTTCTTTGCTTGGCCATTTGCACTGCAATTTGGAGACTTTGATTTGGCATCTTGAAC 660  
 QY 1106 TACAGGACTGGGCAAAAGAGCCCTTGTGCTCAGCCATCAGAGAGTTTGAACAGCCAT 1165  
 DB 661 TACAGGACTGGGCAAAAGAGCCCTTGTGTAGTCAACAGAGAGTTTGAACAGCCAT 720  
 QY 1166 CTTCGCTTGGGCTTTCGTAGCAATACACAGGTGCAAGTGTGTAGAGTCTGCCAAACAG 1225  
 DB 721 CTTCGCTTGGGCTTTCGTAGCAATACATCAGGTGCAAGTGTGTAGAGAGCCCTTGCACAAACAG 780  
 QY 1226 ACCGAATGAATGACTTCTACTGAGTATCAAAAGCATACTTTGATATATAGTTGCC 1285  
 DB 781 ACCGAATGAATGACTTCTACTGAGTATCAAAACATATTTTGAATATAGTTGCC 840

QY 1286 ATGAGCTCTACTTGAACACATCATGATATATGCAAAAATCTAGTGAACCGGACGGC 1345  
 DB 841 ATGAGTCTCTACTTGAACACATATGATATATGCAAAAATCTAGTGAATCCGATCGT 900  
 QY 1346 TCGCGCTCTTCAGGTGGAACAAGAACAGAGCTGTACTCGACCTGTGTTGACAT 1405  
 DB 901 TGTGACCTTTCAGGTGGAACATTAAGAACAGAGGATTAATATTCAGACCTTTTGAAT 960  
 QY 1406 GGGGAGGAAGAGGGAAGGCCATCTTCAAGAAAGCAAGAGATGAGATTTTCCAT 1465  
 DB 961 GGGGAGGAAGAGGGAAGAACCTTCTTCAAGAAAGCAAGAGATTAATTTTCAAT 1020  
 QY 1466 GAGAAAGGATTTGCTGATCAATGACCAAGAGAGCTTTGAACATTTCCATGTC 1525  
 DB 1021 GAGAAAGGATTTGCTGACCAATGACCAAGAGAGCTTTGAACATTTCCATGTC 1080  
 QY 1526 TACGGGACCTTCGCTTTAACAAGGAGTGAACCTGTACACAGGCTACACCAAGAGAAC 1585  
 DB 1081 TATGACAGCCACGCTTTAACAAGAGTGAACCTGTACACAGGCTACACCAAGGAGAAC 1140  
 QY 1586 ATTCTGTATGCCCATATGATGACCGGAGGACCGTATTTGGGTGTGAGATGTGAAC 1645  
 DB 1141 ATCTGTGATGCCCATCTGTACCGAGGACCGTATGATGTGTGAGATGTGAAC 1200  
 QY 1646 AAGATCAGGGGATAGGCGCTTCCAAAGACAGACGAAACAATTCAAGATTTTGTCTGTC 1705  
 DB 1201 AAGATCAGGGGATAGGCGCTTCTTAACAGATGAAACAACTTCAAAATGTTTGTGCGTTC 1260  
 QY 1706 TTCTGCGCATGCGCTTGTGATGCTGTATCATGTACCAAGATTCGCACTCAGATTC 1765  
 DB 1261 TTTTGTGCTTTAGCTTATCATGTGTATATGTATCATAGATTTGCGCATCAGATTC 1320  
 QY 1766 ATCTACAGGATTAACAATGGAAGACTTTCTTACACAGATCTGCACTTCCAGAGTGG 1825  
 DB 1321 ATTTACCGGGATTAACAATGGAAGAGCTGTCTACATAGATTTGTACAGAAAGTGG 1380  
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 DB 1381 CAAAGCTCATGCGCTTCAACCTTCCGAGCTCTTGCAGAAATTAATTAATTCAC 1440  
 QY 1886 TTTGACATTTGCTCTTTCAGAACATGTGGCTGGGATCTTTGTCTACATGATTCATCGG 1945  
 DB 1441 TTTGACATTTGCTCTTTCAGAAACATGTGGCTGGGATTTTGTCTACATGATTCATCGG 1500  
 QY 1946 TCTTGTGGACATCTGTGTTTGAACCTTGAATAATGTGCGCTTTATCATATCTGTGAAG 2005  
 DB 1501 TCTGTGGACATCTGTGTTTGAAGAAAGTGTGTGTATTTATGTCTGTGAAG 1560  
 QY 2006 AAGAACTATCGGGGTTTCTTAACAACAATGGAAGACATGCAAGGAGGACACTGC 2065  
 DB 1561 AAGAACTATCGGGGTTTCTTAACAACAATGGAAGACATGCAAGGAGGACACTGC 1620  
 QY 2066 ATGTATGCAATCTTCAAAACAATAGGCTCTTCAACAGACTCGAGGCAAAAGGCTTG 2125  
 DB 1621 ATGTATGCAATCTTCAAAACAATAGGCTTTTCAACAGACTTGAAGCAAAAGGCTTG 1680  
 QY 2126 CTAAATGCGTGTGTGCAATGACCTGGAACAAGAGGCTTCAAGTAAACAGTACTGACAG 2185  
 DB 1681 CTGAATGCGTGTGTGCAATGACCTGGAACAAGAGGCTTCAAGTAAACAGTACTGACAG 1740  
 QY 2186 AAGTTGACCAACCCCTGCGGCGCTGTACTCACTTCCACATGGAAGCAACCACTTC 2245  
 DB 1741 AAGTTGACCAACCCCTGGAACCGCTCTTCTTCACTTCAACATGGAAGCAACCACTTC 1800  
 QY 2246 TCCCAAGCGGTGTCATCTTTCAGCTGGAAGGCAAAATCTTCTTCAACCTGAGCTTC 2305  
 DB 1801 TCCCAAGCTGTGTCTTCTTCAAGTGTGAAGGCAAAATCTTCTTCAACCTGAGCTTC 1860  
 QY 2306 AGCAGATACAGAGAGGTGTGAGATCATTCGCAAAAGCATCATTCGCAACGACTGCGC 2365  
 DB 1861 AGTGAATATAGCAGAGGTGTGAGATCATTCGCAAAAGCATCATTCGCAACGACTGCGC 1920  
 QY 2366 CTATACTTTGGGAACAAGAAAGCATTTGAGAGATATGACAGACAGGCTGCTGAACCTC 2425



Db 1503 GTCTTTGGCTTTAGCTTACCTGTGCTAATGTATCATAGAAATTCGCACTCAGAG 1562  
Qy 1763 TGCATCTACAGGGTTCACATGAGAAAGCTTCTCTACACAGCATCTGCACTCCAGAG 1822  
Db 1563 TGCATTTACCGGATTAACATGAGAAAGCTGTCTCTACATAGCAATTTGTATCTTCAAGAG 1622  
Qy 1823 TGGCAAGGCTCATGCGCTTCAACCTACGACACGATCTGCGGACATTCAGACTATTC 1882  
Db 1623 TGGCAAGGCTCATGCAATTCACCTCCGCGGCTCTCGAAGAAATTTGAATTAATTC 1682  
Qy 1883 CATTTGACATTTGTCTTTTCAAGAAACATGTGCGCTGAGATCTTTGTCTACATGATTCAT 1942  
Db 1683 CATTTGACATTTGTCTTTTGAAGAAACATGTGCGCTGAGATTTTGTCTACATGATTCAT 1742  
Qy 1943 CGGTCTGTGGGACATCTGTTTGAACCTTGAAGAAATTTGCGGCTTTTATCATGTCTGTG 2002  
Db 1743 CGGTCTGTGGGACATCTGCTTTGAGCTTGAAGAAATTTGTCTTTTATGTCTGTG 1802  
Qy 2003 AAGAAACATATCGCGGCTTCTTACACACATCTGAGACATGCACTGCGTGACAC 2062  
Db 1803 AAGAAACATATCGCGGCTTCTTATCAACATCTGAGACATGCGGTCACTGTAGACAC 1862  
Qy 2063 TGCATGTATGCTCATCTTCAAAACAAATGCGCTCTTCAACAGCTCGAGCGCAAGGC 2122  
Db 1863 TGCATGTATGCTCATCTTCAAAACAAATGCGCTCTTCAACAGCTCGAGCGCAAGGC 1922  
Qy 2123 CTGCTTAATGCGGTCTGTGCTGACATCTGAGACACAGGGGCTTCACTAAGCTACTG 2182  
Db 1923 CTGCTTAATGCGGTCTGTGCTGACATCTGAGACACAGGGGCTTCACTAAGCTACTG 1982  
Qy 2183 CAGAAATTCAGACACCCCTGCGGCTGTATCTCCACCTCCACATGAGACACAC 2242  
Db 1983 CAGAAATTCAGACACCCCTGCGGCTGTATCTCCACCTCCACATGAGACACAC 2042  
Qy 2243 TTCTCCACAGCGGTCTGCTCTTCACTGCTGAGAGGCAATATCTTCTCAGCTGAGC 2302  
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Qy 2303 TCCAGAGATACAGAGAGGCTGAGATCATCGCAAGGCTCATCGCACCGACCTC 2362  
Db 2103 TCCAGAGATACAGAGAGGCTGAGATCATCGCAAGGCTCATCGCACCGACCTC 2162  
Qy 2363 GCCCTTAATCTTTGGGAAACAGGAAGCAGTTGAGAGATGTACAGACAGGGTCTGAGC 2422  
Db 2163 GCCCTTAATCTTTGGGAAACAGGAAGCAGTTGAGAGATGTACAGACAGGGTCTGAGC 2222  
Qy 2423 CTCACACACAGTCCCATGAGACCGGTGATCGGCTTGTATGATGATGCTGCTGATCTT 2482  
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Qy 2483 TGTCTGTGTGACCAACATATGCGCAAGTTACAAATTTGACAGGAAATGATATATGAGAA 2542  
Db 2283 TGTCTGTGTGACCAACATATGCGCAAGTTACAAATTTGACAGGAAATGATATATGAGAA 2342  
Qy 2543 TTCTGGGCTGAGGCTGATGATGAGAAAGCTGAGCACTAGAGCCATTCCTATGATGAGC 2602  
Db 2343 TTCTGGGCTGAGGCTGATGATGAGAAATGAGAAATTTGAGATATCAGGCTATTCCTATGATGAGC 2402  
Qy 2603 AGAGACAAAGGAGATGAGATGCTTCAAGGCAAGCTCGAATTTTCAATGCTGTGCGCAT 2662  
Db 2403 AGAGACAAAGGAGATGAGATGCTTCAAGGCAAGCTCGAATTTTCAATGCTGTGCGCAT 2462  
Qy 2663 CCTGTGTATACACTTGAACGACAGATCTTCCACCCACAGAGCTCTGAGAGGCGCTGC 2722  
Db 2463 CCTGTGTATACACTTGAACGACAGATCTTCCACCCACAGAGCTCTTGAAGAGCATGC 2522  
Qy 2723 AGGATTAATCTCAATCACTGAGGAGAAAGTAAATTCGCGGAGAAAGACAGCATGCTGAT 2782  
Db 2523 AGGATTAATCTCAATCACTGAGGAGAAAGTAAATTCGAGGAGAGAGACATGCACTGAT 2582  
Qy 2783 TCAAGGCCAGGCGCGGCGC 2801

Db 2583 TCAATCCCATCCGTCGCTC 2601  
RESULT 11  
US-10-618-252-3  
Sequence 3, Application US/10618252  
Publication No. US20040018542A1  
GENERAL INFORMATION:  
APPLICANT: Lanfear, Jeremy  
APPLICANT: Robas, Nicola M.  
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
FILE REFERENCE: PC9477B  
CURRENT APPLICATION NUMBER: US/10/618,252  
CURRENT FILING DATE: 2003-07-11  
PRIOR APPLICATION NUMBER: 9826777.6  
PRIOR FILING DATE: 1998-12-04  
PRIOR APPLICATION NUMBER: 9823882.7  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 9811500.9  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 9908247.1  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: 9910801.1  
PRIOR FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 3  
LENGTH: 2798  
TYPE: DNA  
ORGANISM: Human  
US-10-618-252-3  
Query Match 49.6%; Score 1790.2; DB 7; Length 2798;  
Best Local Similarity 86.2%; Pred. No. 0;  
Matches 1981; Conservative 0; Mismatches 318; Indels 0; Gaps 0;  
Qy 503 ACCGATGTTTCTCAGCCCGAGTTTGAACGATGAAAGGTAGAGCCATCTTCTCTC 562  
Db 303 ACCGATGTTTCTCAGAGACAGGTTTGAACGATGAAAGGTAGAGCCATCTTCTCTC 362  
Qy 563 CATCCGAGATATAGATGATATTTGTTCTGAAAGTGTAGTGCAGAGACTGTGAAAG 622  
Db 363 CATCCGAGATATAGATGATATTTGTTCTGAAAGTGTAGTGCAGAGACTGTGAAAG 422  
Qy 623 TGGCTGAGAGGAAACCAACAAAGCAAAAGTAAACATCTTCCAGAGAGTCAAGC 682  
Db 423 TGGCTGAGAGGAAACCAACAAAGTAAACATCTTCCAGAGAGTCAAGC 482  
Qy 683 TACAGATATCGAATATGACAGGAGTCTGTACAGCTGAACGCTAACATAGAGCAGCGC 742  
Db 483 TACAGATATCGAATATGACAGGAGTCTGTATGAACTAAACGCTATATAGAACACG 542  
Qy 743 CTGACACGGGCGGGGACACACCTGCTCTCTATGAGCTCAGACATCATCAGATAT 802  
Db 543 CTGACACGGGCGGGGACACACCTGCTCTCTATGAGCTCAGACATCATCAGATAT 602  
Qy 803 GCCACAAAGCCGAGCTTGTGACTGTACTTCTTGAAGTGCATATATAGCTGTGT 862  
Db 603 GCCACAAAGCCGAGCTTGTGACTGTACTTCTTGAAGTGCATATATAGCTGTGT 662  
Qy 863 GTGTTCATACACCCGAGATGAAAGGACCAACCCCGCTCATCTCTGAGGCGCCATC 922  
Db 663 GTGTTCATACACCCGAGATGAAAGGACCAACCCCGCTCATCTCTGAGGCGCCATC 722  
Qy 923 ACCGAGGATACACATCTCTGCTAGTGGCCAGTCTTAGAGACGTTGTGTAGAG 982  
Db 723 ACTCAGGACACACGCTCTCTGTATGTGGCCAAATTCAGAGAAACATGCTGATAGAA 782  
Qy 983 GATATCTTGGGAGTACAGGATTTCTGAGATCTGCGCTGAGATCAGAACCCGATC 1042  
Db 783 GATATCTTGGGAGTACAGGATTTCTGAGATCTGCGCTGAGATCAGAACCCGATC 842  
Qy 1043 CAGTCTGTTCTTTGCTTGGCCATTTGACATGCACTTGAAGACTTGAATGGCATCTTGA 1102



Db 843 CAGTCTGTTCTTGTCTTACCAATGTCTGCAATGTGACTGTGATGTGATTTCTCGAG 902  
Qy 1103 CTGTACAGGCACTGGGGCAAAAGAGGCTTCTGCTCAGCCATCAGAGAGTTGCAACAGCC 1162  
Db 903 CTGTATCGGCACCTGGGGCAAAAGAGGCTTCTGCTTATGTCAACAGAGGTTGGCAACAGA 962  
Qy 1163 AATCTGTCTTGGGCTCCGTAGCAATACACAGGTGAGTGTGATGAGTCTCGCCAA 1222  
Db 963 AATCTGTCTTGGGCTTCAATGCAATACATCAGGTGAGTGTGATGAGTGTGATGAGT 1022  
Qy 1223 CAGACCGAACTGATATGACTTCTCTACTCGAAGTATCAAGACATCTTGTATATCATAGTT 1282  
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Qy 1283 GGCATGATCTCTCTACTTGAACATCATGATATATGCAAAAAATTTAGTGAACGCCGAC 1342  
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Qy 1343 CGCTGCGGCTCTTCCAGGTGAGCACAAGAAACAAGAGCTGTACTCGGACCTGTTGAC 1402  
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Qy 1403 ATTGGGAGAGAGAGAGAGAGAGAGCCCATCTTCAAGAGACCAAGAGATCAGATTTTCC 1462  
Db 1203 ATTGGATTTCA 1262  
Qy 1463 ATTGATTTCC 1522  
Db 1263 ATTGATTTCC 1322  
Qy 1523 GCTTACGCGGATTTCC 1582  
Db 1323 GCTTATGCAAGATTTCC 1382  
Qy 1583 AACATCTGTGTATGAGCCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1642  
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Qy 1643 AACAGATGATTTCC 1702  
Db 1443 AACAGATGATTTCC 1502  
Qy 1703 GTCCTCTGCGGCACTGGGCTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1762  
Db 1503 GTCCTCTGCGGCACTGGGCTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1562  
Qy 1763 TGCATCTACAGGAGTTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1822  
Db 1563 TGCATCTACAGGAGTTTACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1622  
Qy 1823 TGGCAAGGCTCATGAGGCTTCAACCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1882  
Db 1623 TGGCAAGGCTCATGAGGCTTCAACCTACAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1682  
Qy 1883 CACTTGTGATGAGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1942  
Db 1683 CACTTGTGATGAGGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1742  
Qy 1943 CGGTCTTGTGATTTCC 2002  
Db 1743 CGGTCTGTGATTTCC 1802  
Qy 2003 AAGAGAACTATCGAGGAGTTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2062  
Db 1803 AAGAGAACTATCGAGGAGTTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1862  
Qy 2063 TGCATGATGATTTCC 2122  
Db 1863 TGCATGATGATTTCC 1922  
Qy 2123 CTGCTAATTTGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2182  
Db 2182 CTGCTAATTTGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2182

Db 1923 CTGCTAATTTGCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 1982  
Qy 2183 CAGAGATTTGATTTCC 2242  
Db 1983 CAGAGATTTGATTTCC 2042  
Qy 2243 TTTCTCCAGATTTCC 2302  
Db 2043 TTTCTCCAGATTTCC 2102  
Qy 2303 TTTCTCCAGATTTCC 2362  
Db 2103 TTTCTCCAGATTTCC 2162  
Qy 2363 GGCCTATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2422  
Db 2163 GGCCTATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2222  
Qy 2423 TTTCTCCAGATTTCC 2482  
Db 2223 TTTCTCCAGATTTCC 2282  
Qy 2483 TTTCTCCAGATTTCC 2542  
Db 2283 TTTCTCCAGATTTCC 2342  
Qy 2543 TTTCTCCAGATTTCC 2602  
Db 2343 TTTCTCCAGATTTCC 2402  
Qy 2603 AGATTTCC 2662  
Db 2403 AGATTTCC 2462  
Qy 2663 CTTCTGTGATTTCC 2722  
Db 2463 CTTCTGTGATTTCC 2522  
Qy 2723 AGAGATTAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2782  
Db 2523 AGAGATTAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTTCC 2582  
Qy 2783 TCAGGATTTCC 2842  
Db 2583 TCAGGATTTCC 2602

RESULT 12  
US-10-440-998-5  
; Sequence 5, Application US/10440998  
; Publication No. US20030215919A1  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 2786/35047  
; CURRENT APPLICATION NUMBER: US/10/440,998  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/686,055  
; PRIOR FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3195  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: (67) .. (2403)  
US-10-440-998-5  
Query Match 49.6%; Score 1787.4; DB 6; Length 3195;



Best Local Similarity 86.6%; Pred. No. 0; Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

584 GTTTACGGATGAAAGTGAAGGCTATCTTCTCTCATCCCGAGTATTAGATGAT  
 104 GTTTACGATGAAAGTGAAGGCTATCTTCTCTCATCCCGAGTATTAGATGAT  
 585 TTGTTCTGAAAGTGTAGTGAAGAGCTGTGAAAGTGTGAAAGAGAAACCAACA  
 164 TTGTTCTGAAAGTGTAGTGAAGAGCTGTGAAAGTGTGAAAGAGAAACCAACA  
 645 AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAAGAGATCAAGATTAAGATGAGG  
 224 AATCAAGAAATGAATCGGCTCTTAAGAAAGTCAAGAGATCAAGATTAAGATGAGG  
 705 GAGGTGTGACAGCTGAACAGCTACATAGAGAGAGCTGTGAAAGAGAGAGAGAGAG  
 284 GAGGTGTATATGAATTAACAGCTATATAGAAAGAGAGAGAGAGAGAGAGAGAG  
 765 ACCCTGCTCTATGAGCTCAGAGAGATCAAGATTAAGAGAGAGAGAGAGAGAGAG  
 344 AGCTATCTCTATGAG  
 825 CACTGTAATCTCTGAG  
 404 CACTGTAATCTCTGAG  
 885 AAGAAAGGCAACCCGAGGCTCATCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 464 AAGAAAGGCAACCCGAGGCTCATCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 945 CCTACCTGAGCAAGTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 524 CTATTGTGAGCAAGTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1005 TTCTCTGAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 584 TTCTCAAGAGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1065 TTGTGATGAG  
 644 TTGTGATGAG  
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 704 AAGGCTTCTGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1185 CAATACAG  
 764 CAATACAG  
 1245 TACTGAG  
 824 TACTGAG  
 1305 ACATCATGATATGAG  
 884 ACATCATGATATGAG  
 1365 ACCAAG  
 944 ACCAAG  
 1425 AGCCCATCTTCAAG  
 1004 AACCTGTCTTCAAG  
 1485 AAGTGGCAAG  
 1064 AAGTGGCAAG  
 1545 ACAGGAG

1124 AAGAGAGATGAGATCTTGTACAGAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1605 TGAGCCGAG  
 1184 TGAGCCGAG  
 1665 TGTCCAG  
 1244 TGTCCAG  
 1725 ACTGTCTTACATGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1304 ACTGTCTTACATGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1785 AGAGCTTCTTACATGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1364 AAGAGCTTCTTACATGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
 1845 ACCTACAG  
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 1905 AGAGATGAG  
 1484 AAGAGATGAG  
 1965 TTGAATGAG  
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 2025 CTTCACAG  
 1604 CTTCACAG  
 2085 ACAAGATGAG  
 1664 ACAAGATGAG  
 2145 ATGAGCTGAG  
 1724 ATGAGCTGAG  
 2205 CGGAGCTGAG  
 1784 CGGAGCTGAG  
 2265 TTCAAGTGAAG  
 1844 TTCAAGTGAAG  
 2325 TGAAGATCAG  
 1904 TGAAGATCAG  
 2385 AGAGCTGAG  
 1964 AGAGCTGAG  
 2445 ACCGTGTACAG  
 2024 ACCGTGTACAG  
 2505 CAGTTACAAATTTGAG  
 2084 CAGTTACAAATTTGAG  
 2565 TGAAGAGCTGAG  
 2144 TGAAGAGAGCTGAG  
 2625 CTCAAG  
 2204 CTCAAG

2685 AGATCCCTCCACCCACAGAGCCTCTGTAAGGCTGCAAGGATTAACCTCAATCAGTGGG 2744  
2264 AATCTCTCTCCACGAGGCTCTTCTGAAAGCATGCAAGGATTAATCTCAGTCACTGAGG 2323  
2745 AGAAGGTAATTCGCGGGGAGAGACAGCAATGTGATTTCAAGGCCAGGCCCGCGC 2801  
2324 AGAAGGTGATTCGAGGGGAGAGACTGCACCTGATTTTCATCCCATCCGTGGCTC 2380

RESULT 13  
US-09-420-190-2  
Sequence 2, Application US/09420190  
Patent No. US20020081633A1  
GENERAL INFORMATION:  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Hunter, John Joseph  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: Method for Using 22045, A Human Cyclic  
FILE REFERENCE: 5800-71  
CURRENT APPLICATION NUMBER: US/09/420,190  
CURRENT FILING DATE: 1999-10-18  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 4381  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (67)...(2403)  
US-09-420-190-2

Query Match 49.6%; Score 1787.4; DB 3; Length 4381;  
Best Local Similarity 86.6%; Pred. No. 0;  
Matches 191; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

525 GTTTACCGGATGAAAAGTGAAGGCTATCTTCTCCATCCCGGATTAAGTGAAT 584  
104 GTTTGACAGATGAAAAGTGAAGGCAATCTTCTCTTCACCCCCGATTAAGTGAAT 163  
585 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGTGAGAGAGAAAACCA 644  
164 TTGTATCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGTGAGAGAGAAAACCA 223  
645 AAGCAAAAGATGAAACATCTCCCAAGAAAGTCAAGAGTACCAAGATGAAATATG 704  
224 AATCAGAAATGAAATCGCTCTCAAGAAAGTCAAGAGTACCAAGATGAAATATG 283  
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825 CACTGTACTCTCTGAGAGTCAATATAGCTGTGTGTGTTCAATACACCCGGAGTA 884  
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DB 1784 CGGCTTCTACTCACTTCCACATGAGACACCACTTCTCCAGACTGTGTCAATCC 1843
QY 2265 TTCACTGGAGAGGCAATATCTTCTCCACCTGAGCTCCAGAGTACAGAGAGTGC 2324
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## RESULT 14

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; Sequence 2, Application US/10458839
; Publication No. US20030215898A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/10/458,839
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/09/420,190
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 4381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(2403)
US-10-458-839-2

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Query Match 49.6%; Score 1787.4; DB 6; Length 4381;  
Best Local Similarity 86.6%; Pred. No. 0;

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QY 585 TTGTTTGAAGTGTATGTCAGAGACTGTGAAAATGTGCTGAAGAGAAACCAACA 644
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RESULT 15  
US-10-440-998-1  
Sequence 1, Application US/10440998  
Publication No. US20030215919A1  
GENERAL INFORMATION:  
APPLICANT: Loughney, Kate  
TITLE OF INVENTION: Phosphodiesterase 8A  
FILE REFERENCE: 27866/35047  
CURRENT APPLICATION NUMBER: US/10/440,998  
CURRENT FILING DATE: 2003-05-19  
PRIOR APPLICATION NUMBER: US/09/686,055  
PRIOR FILING DATE: 2000-10-11  
PRIOR APPLICATION NUMBER: 08/951,648  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2298  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(2298)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (868)..(870)  
OTHER INFORMATION: The amino acid encoded by nucleotides 868-870 is  
OTHER INFORMATION: either Pro or Leu  
US-10-440-998-1

Query Match 49.5%; Score 1785; DB 6; Length 2298;  
Best Local Similarity 86.5%; Pred. No. 0; Mismatches 306; Indels 0; Gaps 0;  
Matches 1968; Conservative 1;

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 Job time : 2733 secs

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Db 312 GCTTCGGAAGGCTGACCGAGTCTTCTCAGGCCCAAGTTGACGATGAAAAAGTGAAG 371  
Qy 549 CCTATCTTCTCTCCATCCCGAGGTATTGATGAATTTGTTTCTGAAGTTTATGTCAG 608  
Db 372 CCTATCTTCTCTCCATCCCGAGGTATTGACGAGTTGTTCTGAAAGTGTATGTCGCG 431  
Qy 609 AGACGTGGAAGAGTGGCTGAAGAGAAAAACCAACAAAGCAAAAGATGAACATCTCCA 668  
Db 432 AGACGTGGAAGAGTGGCTGAAGAGAAAAACCAACAAAGCAAAAGATGAACATCTCTA 491  
Qy 669 AGGAAGTCAGCAGGTACAGAGATACGAATATGCAAGGAGTCTGTATCGAGCTGAACAGCT 728  
Db 492 AGGAAGTCAGCAGGTACAGAGACAGAAATGCAAGGAGTCTGTATCGAGCTGAACAGCT 551  
Qy 729 ACATAGAGACGCGCTGGAACAGGCGGGGGAACAACACTGCTCCTCTATGAGCTCAGCA 788  
Db 552 ACATAGAGACGCGCTGGAACAGGCGGGGGAACAACACTGCTCCTCTATGAGCTAAGCA 611  
Qy 789 GCATCATCAGATTAACCAACAAAGCGAAGGATTGCACTGTACTTCCCTTGAAGTGA 848  
Db 612 GTATCATCAGATTAACCAACAAAGCGAAGTGAAGTGAAGTGAAGTGAAGTGA 671  
Qy 849 ATTAATAGCCTGTGTGTGTTATATCAACCCGAGATGAAGGAAGCCACCCGCTCATATCC 908  
Db 672 ATTAATAGTGTGTGTGTTATATCAACCCGAGATGAAGGAAGTGAAGCCGCTCATATCC 731  
Qy 909 CTGCAAGGCGCCATCAACCAAGGGTACCAACATCTTCTGCTTAAGTGCACATGTAGAGAGA 968  
Db 732 CCGCAGGGGCCATCAACCAAGGGGACCAACATCTTCTGCTTAAGTGCACATGTAGAGAGA 791  
Qy 969 CGTTTGTGTAAGATTAATCTTGGGGAAGAGCAATTCCTGAGGTAATGAGCTGAGAT 1028  
Db 792 CCTCTGCTGTAAGACATCTTGGGGAAGAGCAATTCCTGAGGCACTGAGTCTGAGAT 851  
Qy 1029 CAGGAACCCGACATCAAGTCTGTCTTGTGCTTCCCATGTCATGCACTGAGACTTGA 1088  
Db 852 CAGGAACCCGATTCAGTCTGTCTTGTGCTTCCCATGTCATGCACTGAGACTTGA 911  
Qy 1089 TTGCATCTCTGAACCTGTAACAGCACTGAGGCAAAAGAGGCTTCTGCTCAGCCATCAG 1148  
Db 912 TTGCATCTCTGAACCTGTAACAGCACTGAGGCAAAAGAGGCTTCTGCTCAGCCATCAG 971  
Qy 1149 AGTTTGCAAGCCCAATCTTGTGGGCTTCCGTAGCAATACCAAGGTCAGAGTGTGA 1208  
Db 972 AGTTTGCAAGCCCAATCTGCTGGGCTTCCGTAGCAATACCAAGGTCAGAGTGTGA 1031  
Qy 1209 GAGGTCTGCGCAAAAGACCGAATGAATGACTTCTCGACGTATCAAGACATTA 1268  
Db 1032 GAGGTCTGCGCAAGACCGAATGAATGACTTCTGCTCGATGTATCAAGACATTA 1091  
Qy 1269 TTGATTAACATAGTTGCCATAGACTCTCTATCTTGAACATCAATGATATGCAAAAAATC 1328  
Db 1092 TTGATTAACATAGTTGCCATAGACTCTCTATCTTGAACATCAATGATATGCAAAAAATC 1151  
Qy 1329 TAGTGAAGCGCGACCGCTGCGGCTTCTCAGGTGAACCAAGAAACAGAGGCTGTACT 1388  
Db 1152 TAGTGAAGCGCGACCGCTGCGGCTTCTCAGGTGAACCAAGAAACAGAGGCTGTACT 1211  
Qy 1389 CGGACCTGTTTGAATTTGGGAGAGAAAGAGGGGAAGCCCATCTTCAAGAAAGCAAG 1448  
Db 1212 CGGACCTGTTTGAATTTGGGAGAGAAAGAGGGGAAGCCCATCTTCAAGAAAGCAAG 1271  
Qy 1449 AGATCAGATTTTCAATTTGAAGAAAGGATTGCTGCTCAAGTGGCAAGAACGCGAATCT 1508  
Db 1272 AGATCAGATTTTCAATTTGAAGAAAGGATTGCTGCTCAAGTGGCAAGAACGCGAATCT 1331  
Qy 1509 TGAACATTTCCGATGCTTACGGGAACTCTGCTTTTAAAGGAGGTGAGACTGTACAG 1568  
Db 1332 TGAACATTTCCGATGCTTACGGGAACTCTGCTTTTAAAGGAGGTGAGACTGTACAG 1391  
Qy 1569 GCTACCAACGAGGAACATTTCTGTATGCCATAGTGAAGGCAAGGCAAGTGTAGCG 1628  
L

Db 1392 GCTATACCAACCGGAACATTTCTGTGTATGCCATAGTGAAGCCGCGAGCGTGAATCGGTG 1451  
Qy 1629 TGTGTGACATGTGTGAACAAAGATCAGCGGTAGAGCCCTTCTCAAGACAGACGAACAAT 1688  
Db 1452 TGTGTGACATGTGTGAACAAAGATCAGCGGTAGAGCCCTTCTCAAGACGAATGAACAAT 1511  
Qy 1689 TCAAGATGTTTGTCTTCTTGTGCGCATGAGCTTGGCACTGTGTCTTAACATGAACAGAGA 1748  
Db 1512 TCAAGATGTTTGTCTTCTTGTGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCG 1571  
Qy 1749 TCCGCACTCAGAAATGCACTTACAGGTTTACATGGAAGACTTTTCTTCAACACAGACT 1808  
Db 1572 TCCGCACTCAGAAATGCACTTACAGGTTTACATGGAAGACTTTTCTTCAACACAGACT 1631  
Qy 1809 GCACTCCGAGAGAGGGAAGGCCCTACAGGCTTCAACCTTCAAGACAGCATCTGCGGAG 1868  
Db 1632 GCACTCCGAGAGAGGGAAGGCCCTACAGGCTTCAACCTTCAAGACAGCATCTGCGGAG 1691  
Qy 1869 ACATGAGCTATTTCCATTTTGAACATTTGCTCTTCAAGACAGCATCTGCGGAGCTTTTG 1928  
Db 1692 ACATGAGCTATTTCCATTTTGAACATTTGCTCTTCAAGACAGCATCTGCGGAGCTTTTG 1751  
Qy 1929 TCTACATGATTCATGCTGCTTGTGGGACATCTGTTTGAACCTTGAACATTTGCTGCT 1988  
Db 1752 TCTACATGATTCATGCTGCTTGTGGGACATCTGTTTGAACCTTGAACATTTGCTGCT 1811  
Qy 1989 TTAATATCTCTGTGAAGAACTTATGCGGCTTCTTCAACATGGAAGCATGCGAG 2048  
Db 1812 TTAATATCTCTGTGAAGAACTTATGCGGCTTCTTCAACATGGAAGCATGCGAG 1871  
Qy 2049 TCACGAGTGCACATGATGATGCAATCTTCAACAAACAAATGAGCTCTTCAACAGAC 2108  
Db 1872 TCACGAGTGCACATGATGATGCAATCTTCAACAAACAAATGAGCTCTTCAACAGAC 1931  
Qy 2109 TCGACGGAAGAGGCTGCTTAATGCTGTCTGTGTCATGACTTGAACAGAGGCTTCA 2168  
Db 1932 TCGACGGAAGAGGCTGCTTAATGCTGTCTGTGTCATGACTTGAACAGAGGCTTCA 1991  
Qy 2169 GTTAACGCTACCTGGAAGATTCGACCAACCCCTGGGCGGCTGTACTCACTTCACCA 2228  
Db 1992 GTTAACGCTACCTGGAAGATTCGACCAACCCCTGGGCGGCTGTACTCACTTCACCA 2051  
Qy 2229 TGGAGCAACCACTTCTCCAGACGAGTGCATCTTCAAGTGAAGAGCAACATCT 2288  
Db 2052 TGGAGCAACCACTTCTCCAGACGAGTGCATCTTCAAGTGAAGAGCAACATCT 2111  
Qy 2289 TCTCCACCTTGAAGCTCAGGAGTACGACAGGTGCTGGAATCATCTCCGAAGCATCA 2348  
Db 2112 TCTCCACCTTGAAGCTCAGGAGTACGACAGGTGCTGGAATCATCTCCGAAGCATCA 2171  
Qy 2349 TCGCACCGAAGCTGCGCTTATCTTGGGAAACAGAAACAGTTGAGAGATGTACAGA 2408  
Db 2172 TCGCACCGAAGCTGCGCTTATCTTGGGAAACAGAAACAGTTGAGAGATGTACAGA 2231  
Qy 2409 CAGGTCGCTGAACCTTCCACAAACAGTCCCATTCGAGACCGTGTCACTCGGCTTGAATGA 2468  
Db 2232 CAGGTCGCTGAACCTTCCACAAACAGTCCCATTCGAGACCGGCTGTCACTCGGCTTGAATGA 2291  
Qy 2469 CTGCTGTGATCTTGTCTCTGTGACAAACTATGAGCAATGACAAATTTGACAGGAAATG 2528  
Db 2292 CTGCTGTGATCTTGTCTCTGTGACAAACTATGAGCAATGACAAATTTGACAGGAAATG 2351  
Qy 2529 ATATATATGCAAGATTTCTGGGCTGAGGATGATGAAATGAAGCTGGGCAATACAGCCCA 2588  
Db 2352 ATATATATGCAAGATTTCTGGGCTGAGGATGATGAAATGAAGATTTGGGATACAGCCCA 2411  
Qy 2589 TTCCATATATGAGACAGACAGAGATGAAAGTCCCTCAAGGAGAGCTCGGATTTCTCA 2648  
Db 2412 TTCCATATATGAGACAGACAGAGATGAAAGTCCCTCAAGGAGAGCTCGGATTTCTCA 2471  
Qy 2649 ATGCTGTGCGCAATTCCTGTATACCACTTGAAGCAGATCTTCCACCAAGAGCTTC 2708  
Db 2472 ATGCTGTGCGCAATTCCTGTATACCACTTGAAGCAGATCTTCCACCAAGAGCTTC 2531







APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46027  
LENGTH: 2163  
TYPE: DNA  
ORGANISM: Bovine 19866880431658  
US-10-750-185-46027

Query Match 4.1%; Score 146.2; DB 6; Length 2163;  
Best Local Similarity 87.4%; Pred. No. 4.1e-25;  
Matches 160; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2260 CATCTTCAGCTGGAAGGCGACAATATCTTCCACCCCTGAGCTCCAGGAGTAGAGCA 2319  
DB 1275 CTTCCTTGAAGGCGACAACATCTTCCACCCCTGAGCTCCAGGAGTAGAGCA 1216  
QY 2320 GGTGCTGAGATCATCCGCAAGCCATCATCCGCCAGCTCGCCCTTACTTTGGGA 2379  
DB 1215 GGTGCTGAGATCATCCGCAAGCCATCATCCGCCAGCTCGCCCTTACTTTGGGA 1156  
QY 2380 CAGGAAGAGTTGAGAGATGTACAGACAGGGTGTGCTGAACTTCCACACCACTGCCA 2439  
DB 1155 CCGGAAGCAGCTGGAAGAGATGTACAGACTGGGTGCTGAACTTAATTAACCAATCACA 1096  
QY 2440 TCG 2442  
DB 1095 TAG 1093

RESULT 7  
US-10-750-623-46027/c  
Sequence 46027, Application US/10750623  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46027  
LENGTH: 2163  
TYPE: DNA  
ORGANISM: Bovine 19866880431658  
US-10-750-623-46027

Query Match 4.1%; Score 146.2; DB 6; Length 2163;  
Best Local Similarity 87.4%; Pred. No. 4.1e-25;  
Matches 160; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 2260 CATCTTCAGCTGGAAGGCGACAATATCTTCCACCCCTGAGCTCCAGGAGTAGAGCA 2319

DB 1275 CTTCCTTGAAGGCGACAACATCTTCCACCCCTGAGCTCCAGGAGTAGAGCA 1216  
QY 2320 GGTGCTGAGATCATCCGCAAGCCATCATCCGCCAGCTCGCCCTTACTTTGGGA 2379  
DB 1215 GGTGCTGAGATCATCCGCAAGCCATCATCCGCCAGCTCGCCCTTACTTTGGGA 1156  
QY 2380 CAGGAAGAGTTGAGAGATGTACAGACAGGGTGTGCTGAACTTCCACACCACTGCCA 2439  
DB 1155 CCGGAAGCAGCTGGAAGAGATGTACAGACTGGGTGCTGAACTTAATTAACCAATCACA 1096  
QY 2440 TCG 2442  
DB 1095 TAG 1093

RESULT 8  
US-10-750-185-46028  
Sequence 46028, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46028  
LENGTH: 764  
TYPE: DNA  
ORGANISM: Bovine 19866880722444  
US-10-750-185-46028

Query Match 2.0%; Score 72.8; DB 6; Length 764;  
Best Local Similarity 87.0%; Pred. No. 9.7e-08;  
Matches 80; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1960 CTGTTTGAAGTGAATAATGTGCGTTTATCATGCTGTGAAGAACTATCGCG 2019  
DB 673 CAGCTTCAGCTGAGAGAGTGTGCGTTTCATCATGTGTGAAGAACTATCGCG 732  
QY 2020 GGTTCCTTACCAACAATGGAAGCATGCA 2051  
DB 733 GGTTCCTTACCAACAATGGAAGCATGCGTGA 764

RESULT 9  
US-10-750-623-46028  
Sequence 46028, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31



NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 46028  
LENGTH: 764  
TYPE: DNA  
ORGANISM: Bovine 1986680722444  
US-10-750-623-46028

Query Match  
Best Local Similarity 87.0%; Score 72.8; DB 6; Length 764;  
Matches 80; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

1960 CTGTTTGAAGTGAATAATGTCCTTTATCATGCTGTGAAGAAGATATATGCGG 2019  
673 CAGCTTCGAGCTGAGAGAGTGTGCGTTTCATCATGCTGTGAAGAAGATATATGCGG 732  
2020 GGTTCCTTACCAACTGAGAGATGATGATCA 2051  
733 GGTTCCTTACCAACTGAGAGATGATGATGATG 764

RESULT 10  
US-11-075-185-35

Sequence 35, Application US/11075185  
Publication No. US20050266434A1  
GENERAL INFORMATION:  
APPLICANT: REEVES, CHRISTOPHER D  
APPLICANT: JULIEN, BRYAN  
APPLICANT: REID, RALPH  
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMERUTICINS  
FILE REFERENCE: 010099.03  
CURRENT APPLICATION NUMBER: US/11/075.185  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/551,103  
PRIOR FILING DATE: 2004-03-08  
PRIOR APPLICATION NUMBER: US 60/568,290  
PRIOR FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 35  
LENGTH: 10968  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-11-075-185-35

Query Match  
Best Local Similarity 47.8%; Score 58.8; DB 7; Length 10968;  
Matches 171; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

57 GCGCAGCGCGGCTGAG 116  
8467 GCGCGGAG 8526  
117 GAG 176  
8527 GCGCGGAG 8586  
177 GTGCGAG 236  
8587 CTCACAGCGCGGCTACAG 8646  
237 GCTTGTGCTCTCCCTGCG 296  
8647 GCGGTGCGCGAG 8706  
297 ACCCGGAG 356  
8707 GCGGTGCGCGAG 8766  
357 GCGTGGCG 414  
8767 CACTGCTGTGCTGCG 8824

RESULT 11  
US-11-075-185-1

Sequence 1, Application US/11075185  
Publication No. US20050266434A1  
GENERAL INFORMATION:  
APPLICANT: REEVES, CHRISTOPHER D  
APPLICANT: JULIEN, BRYAN  
APPLICANT: REID, RALPH  
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMERUTICINS  
FILE REFERENCE: 010099.03  
CURRENT APPLICATION NUMBER: US/11/075.185  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/551,103  
PRIOR FILING DATE: 2004-03-08  
PRIOR APPLICATION NUMBER: US 60/568,290  
PRIOR FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 1  
LENGTH: 78869  
TYPE: DNA  
ORGANISM: Sorangium cellulosum  
US-11-075-185-1

Query Match  
Best Local Similarity 47.8%; Score 58.8; DB 7; Length 78869;  
Matches 171; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

57 GCGCAGCGCGGCTGAG 116  
23734 GCGCGGAG 23793  
117 GAG 176  
23794 GCGCGGAG 23853  
177 GTGCGAG 236  
23854 CTCACAGCGCGGCTACAG 23913  
237 GCTTGTGCTCTCCCTGCG 236  
23914 GCGGTGCGCGAG 23973  
297 ACCCGGAG 356  
23974 GCGGTGCGCGAG 24033  
357 GCGTGGCG 414  
24034 CACTGCTGTGCTGCG 24091

RESULT 12  
US-10-453-372-659/c

Sequence 659, Application US/10453372  
Publication No. US20060003323A1  
GENERAL INFORMATION:  
APPLICANT: Aleobrook, et al.  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS  
FILE REFERENCE: 21402-589 A  
CURRENT APPLICATION NUMBER: US/10/453.372  
CURRENT FILING DATE: 2003-06-03  
PRIOR APPLICATION NUMBER: 09/789390  
PRIOR FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/185967  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: 09/823187  
PRIOR FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/195792  
PRIOR FILING DATE: 2000-03-10  
PRIOR APPLICATION NUMBER: 09/839446





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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 10, 2006, 13:48:45 ; Search time 81 Seconds  
(without alignments)  
4317.846 Million cell updates/sec

Title: US-10-618-252-15  
Perfect score: 4206  
Sequence: 1 MEDGSPNNASCFRRLTECF.....GGPAPSKSTPBKLVKVED 796

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: \_Geneseq\_21:\*
  - 2: geneseqp1980s:\*
  - 3: geneseqp1990s:\*
  - 4: geneseqp2000s:\*
  - 5: geneseqp2001s:\*
  - 6: geneseqp2002s:\*
  - 7: geneseqp2003as:\*
  - 8: geneseqp2003bs:\*
  - 9: geneseqp2004s:\*
  - 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	4206	100.0	796	3	AAV53940 AAY53940 A murine
2	4198	99.8	796	3	ADT92234 Mouse PDE
3	4123	98.0	794	3	AAAB26855 Human pho
4	4123	98.0	794	3	ADT92235 Rat PDE10
5	4080	97.0	779	8	ADT92238 Mouse PDE
6	4078.5	97.0	797	8	ADT92217 Murine ph
7	4072	96.8	790	8	ADT92236 Mouse PDB
8	4012.5	95.4	795	8	ADT92219 Rat phosp
9	4004	95.2	789	3	AAAB26854 Human pho
10	4004	95.2	789	3	ADT92233 Human PDE
11	3997	95.0	788	3	AAAB26856 Human pho
12	3997	95.0	803	2	ADT92237 Rat PDE10
13	3997	95.0	803	2	AAV13935 Human pho
14	3997	95.0	803	4	AAAB28257 Human pho
15	3997	95.0	803	7	AAE39535 Human pho
16	3997	95.0	803	4	ADM34018 Human pho
17	3993	94.9	789	3	AAV53935 Human P
18	3951.5	93.9	773	6	ABR42040 Rat phosp
19	3880	92.2	806	4	AAAM51617 Human PDE
20	3878	92.2	779	2	AAV13936 Human pho
21	3878	92.2	779	3	AAAB26853 Human pho
22	3878	92.2	779	4	AAAB28258 Human pho
23	3878	92.2	779	4	AAAB73486 Human cyc
24	3878	92.2	779	7	AAE39536 Human pho

25	3878	92.2	779	8	ADM34020 Human pho
26	3878	92.2	779	8	ADO36626 Human pho
27	3878	92.2	779	8	ADR46243 Human pho
28	3878	92.2	779	8	ADT92232 Human PDE
29	3878	92.2	779	9	AEAB69222 Human mod
30	3873	92.1	766	2	AAV13934 Human pho
31	3873	92.1	766	4	AAAB28256 Human pho
32	3873	92.1	766	7	AAE39534 Human pho
33	3873	92.1	766	8	ADM34016 Human pho
34	3867	91.9	791	3	AAV53936 A human p
35	3815	90.7	759	3	AAV53936 Amino ac
36	3815	90.7	767	3	AAV53963 Formula V
37	3808	90.5	754	3	AAV53961 Formula V
38	3798.5	90.3	758	3	AAV53962 Formula V
39	3796	90.3	774	3	AAV57306 Rat phosp
40	3790	90.1	749	3	AAV53959 Formula I
41	3790	90.1	750	3	AAV53960 Formula I
42	1726	41.0	329	9	ADY50217 Human PDB
43	1726	41.0	329	9	ADZ46773 Human PDB
44	1710	40.7	339	8	ADR46245 Human pho
45	1692	40.2	327	8	ADR46247 Human pho

ALIGNMENTS

RESULT 1  
AAV53940  
ID AAV53940 standard; protein; 796 AA.  
XX  
AC AAV53940;  
XX  
DT 13-MAR-2000 (first entry)  
XX  
DE A murine phosphodiesterase enzyme designated PDE11.  
XX  
KW Phosphodiesterase enzyme; PDE11; cGMP; GMP; male erectile process;  
KW sexual dysfunction; PDE11 imbalance.  
OS  
XX Mus sp.  
XX  
PN EP967284-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 21-MAY-1999; 99EP-00303985.  
XX  
PR 28-MAY-1998; 98GB-00011500.  
PR 30-OCT-1998; 98GB-00023882.  
PR 04-DEC-1998; 98GB-00026777.  
PR 09-APR-1999; 99GB-00008247.  
PR 10-MAY-1999; 99GB-00010801.  
XX  
PA (PF1Z ) PFIZER LTD.  
PA (PF1Z ) PFIZER INC.  
PI Lanfear J, Robas NM;  
PI WPI; 2000-064614/06.  
DR N-PSDB; AAZ26971.  
XX  
XX Novel polypeptides and polynucleotides used to identify agents which  
PT modulate phosphodiesterase activity.  
PS Example 8; Page 70-74; 158p; English.  
CC The present sequence represents a murine phosphodiesterase enzyme,  
CC designated PDE11. PDE11 sequences from human and rat are also disclosed.  
CC PDE11 is found in the striatum and corpus cavernosum. PDE11 is believed  
CC to catalyze the conversion of cGMP to GMP. As cGMP is the messenger in  
CC the male erectile process, inhibiting the activity of PDE11 is likely to  
CC increase the concentration of cGMP and so enhance the male erectile  
CC process. The PDE11 enzymes are used in assays for identifying agents

CC which can affect PDE11 activity or expression. They are also used to  
CC screen for agents useful in the treatment of sexual dysfunction. The  
CC identified agent can be used in a pharmaceutical compositions to treat a  
CC disease or condition associated with PDE11. A PDE11 gene or expression  
CC product can be used to prepare a medicament for the treatment or  
CC modulation of disturbances associated with a PDE11 imbalance. The gene or  
CC expression product can also be used to screen for modulators of PDE11  
CC activity or expression

**SQ** Sequence 796 AA;

Query Match	100.0%;	Score 4206;	DB 3;	Length 796;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 796;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MEDGSPNNASCFRRRLTECFLSBPSLTDEKVKAYLSLHPVULDFVSESVSAEIVYKMLKRX	60
Db	1	MEDGSPNNASCFRRRLTECFLSBPSLTDEKVKAYLSLHPVULDFVSESVSAEIVYKMLKRX	60
Qy	61	TNKKADSPSPAEVRYODTNMGVVYELNSYIEBOLDPGGDHLLLYELSSITIRLATKAD	120
Db	61	TNKKADSPSPAEVRYODTNMGVVYELNSYIEBOLDPGGDHLLLYELSSITIRLATKAD	120
Qy	121	GFALYFJGECNNSLCVFIIPGMEKGQPRLLIPAGPIITOGITISAVYAKSRKTLLEDIIGD	180
Db	121	GFALYFJGECNNSLCVFIIPGMEKGQPRLLIPAGPIITOGITISAVYAKSRKTLLEDIIGD	180
Qy	181	ERFRRGJGEBGTRTQSVLCPIRYTAIDDLGILELYHHMGWEACLSHQBVAATNLAMA	240
Db	181	ERFRRGJGEBGTRTQSVLCPIRYTAIDDLGILELYHHMGWEACLSHQBVAATNLAMA	240
Qy	241	SVALHVOVCGKGLAKQETELNDFLLDVSRTYEPDNIAVISLSEHIMITYAKNLVNAADRCALF	300
Db	241	SVALHVOVCGKGLAKQETELNDFLLDVSRTYEPDNIAVISLSEHIMITYAKNLVNAADRCALF	300
Qy	301	QVDHKNKELYSDFDIGEKEGKPIFKTKYKEIRFSIEKGJAGQVARTGEVLNI PDAYADP	360
Db	301	QVDHKNKELYSDFDIGEKEGKPIFKTKYKEIRFSIEKGJAGQVARTGEVLNI PDAYADP	360
Qy	361	RPNREVDLYGYTTRNLICMPRIVSGSVIYGVQWVNKISGSAFSTDDNNPMPFVAPCAL	420
Db	361	RPNREVDLYGYTTRNLICMPRIVSGSVIYGVQWVNKISGSAFSTDDNNPMPFVAPCAL	420
Qy	421	ALHCANNYHRIHSECIYRVYMEKLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIG	480
Db	421	ALHCANNYHRIHSECIYRVYMEKLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIG	480
Qy	481	PPENNMPGIFVYMTIHRSCGISCFELEKLCRPIFMSYKQYRRVRYNNMKAUTVAHCMTAI	540
Db	481	PPENNMPGIFVYMTIHRSCGISCFELEKLCRPIFMSYKQYRRVRYNNMKAUTVAHCMTAI	540
Qy	541	LÖNNNGJFTDERRKGLIACFCHDLDHGFNSYIÖKDHPILAAIYSTTMEÖHHSOTV	600
Db	541	LÖNNNGJFTDERRKGLIACFCHDLDHGFNSYIÖKDHPILAAIYSTTMEÖHHSOTV	600
Qy	601	SILÖBEGHNFSTLSSSEYEQVLEIRKAIJATDLATFYGNRKÖLEMYQÖTSLMHNÖS	660
Db	601	SILÖBEGHNFSTLSSSEYEQVLEIRKAIJATDLATFYGNRKÖLEMYQÖTSLMHNÖS	660
Qy	661	HRDRAVIGLMTATCDLCSYTKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDXRD	720
Db	661	HRDRAVIGLMTATCDLCSYTKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDXRD	720
Qy	721	EVPGGÖGJGFNAVAIIPCTYTLTOLILPTEPRLPKCRDULNÖMEKVIROBETAMTISGQGP	780
Db	721	EVPGGÖGJGFNAVAIIPCTYTLTOLILPTEPRLPKCRDULNÖMEKVIROBETAMTISGQGP	780
Qy	781	APSKESTEKLNVKVED 796	
Db	781	APSKESTEKLNVKVED 796	
RESULT 2			

ADT92234  
ID ADT92234 standard; protein; 796 AA.

AC ADT92234;

DT 13-JAN-2005 (first entry)

DE Mouse PDE10A2 isoform sequence.

KM PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic; neuroprotective; gene therapy; transgenic; PDE10A2; mouse

OS Mus musculus.

PN WO2004090126-A2.

PD 21-OCT-2004.

PF 30-MAR-2004; 2004WO-US009878.

PR 03-APR-2003; 2003US-0459603P.

PA (MEMO-) MEMORY PHARM CORP.

PI Wang D, Bugaj-Gaweda B;

DR WPI; 2004-748763/73.

PT New isolated polynucleotide comprising a polynucleotide sequence coding

PT treating or preventing memory, psychiatric or cognitive disorders.

PS Disclosure; SEQ ID NO 19; 93pp; English.

CC The invention relates polynucleotide sequences coding for mammalian

CC Identifying an agent that modulates the expression or activity of a

CC measuring amounts of cAMP or cGMP produced in the presence of the agent.

CC The polynucleotides are useful in diagnostic assays and for screening.

CC treating or preventing memory, psychiatric or cognitive disorders.

CC used in a comparison study with the murine and rat PDE10A7 sequences.

**SQ Sequence 796 AA;**

Query Match 99.8%; Score 4198; DB 8; Length 796;

Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MEDQSPNNASGCFRRLLTSCFLSPSLTDEKRYAYLSLHPOULDEPVSSEVSATYKMLTRK	60
Db	1	MEDQSPNNASGCFRRLLTSCFLSPSLTDEKRYAYLSLHPOULDEPVSSEVSATYKMLTRK	60
QY	61	TNKKADDESPKEVSRYODTNMQGVVYELNSYIEGRLLDTGDNHLLYELSSIIIRIATKAD	120
Db	61	TNKKADDESPKEVSRYODTNMQGVVYELNSYIEGRLLDTGDNHLLYELSSIIIRIATKAD	120
QY	121	GFALYPIFGECNNSLCVFIPIQMGMEGQRLIPAGITIGQTTISAVVAASKRTLVEDLIGD	180
QY	121	GFALYPIFGECNNSLCVFIPIQMGMEGQRLIPAGITIGQTTISAVVAASKRTLVEDLIGD	180
Db	121	GFALYPIFGECNNSLCVFIPIQMGMEGQRLIPAGITIGQTTISAVVAASKRTLVEDLIGD	180
QY	181	ERPERGTGLSEGTRIQSVLCPIYTAIGDLIGLIELRYHMGKEAFCLSHOEVAATANTAMA	240
Db	181	ERPERGTGLSEGTRIQSVLCPIYTAIGDLIGLIELRYHMGKEAFCLSHOEVAATANTAMA	240
QY	241	SVALHVOVCRGLAKOTELNDFLIDVSKTPEDNTVAIDSLLEHMTIAYKULVYNDRCALF	300
Db	241	SVALHVOVCRGLAKOTELNDFLIDVSKTYFDNTVAIDSLLEHMTIAYKULVYNDRCALF	300
QY	301	QVDHKNELYSDFLDEIEKEGKQPIFKKTYEIRFSIEKGIAGQAVARTGEVLTINDPAYADP	360



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Db      |||||
301 QVDHKNKELYSDFIGEEKSGPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYADP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSGVIGVQMNKISGSAFSGKTDENNFMFAVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSGVIGVQMNKISGSAFSGKTDENNFMFAVFCAL 420
Qy      421 ALHCANMTHRIHSECTIYRVMEKLSYHSICTSEEWQGLMRNLPARICRDIELFFPDIG 480
Db      421 ALHCANMTHRIHSECTIYRVMEKLSYHSICTSEEWQGLMRNLPARICRDIELFFPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRRVRYNNMKAAVVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRRVRYNNMKAAVVAHCMYAI 540
Qy      541 LQNNNGLPFTDLERKGLIACLDHLDHGRFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Db      541 LQNNNGLPFTDLERKGLIACLDHLDHGRFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Qy      601 SILOEGHNIFFSTLSSEYEYQVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Db      601 SILOEGHNIFFSTLSSEYEYQVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Qy      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXD 720
Db      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXD 720
Qy      721 EYPOGQLGFYNAVAIPCYTTLTQILPTEPPLKACADNINQWEKVI RGETAMWISGPGP 780
Db      721 EYPOGQLGFYNAVAIPCYTTLTQILPTEPPLKACADNINQWEKVI RGETAMWISGPGP 780
Qy      781 APSKSTPEKLANVKVED 796
Db      781 APSKSTPEKLANVKVED 796

RESULT 3
AAB26855
ID AAB26855 standard; protein; 794 AA.
XX
AC AAB26855;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human phosphodiesterase 10 (PDE10) amino acid sequence 3.
XX
KM Phosphodiesterase 10; PDE10; human.
XX
OS Homo sapiens.
XX
PN JP2000224992-A.
XX
PD 15-AUG-2000.
XX
PF 11-MAY-1999; 99JP-00129343.
XX
PR 30-NOV-1998; 98JP-00338861.
XX
PA (TANA ) TANABE SEIYAKU CO.
XX
DR MPI; 2000-605129/58.
XX
DR N-PSDB; AAA09591.
XX
PT Novel phosphodiesterase and its gene for research on complex mechanism of
PT intracellular information transfer.
PS Disclosure; Page 20-23; 29pp; Japanese.
XX
CC Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
XX proteins AAB26853-826856. Phosphodiesterase 10 and its gene are useful
XX for research on the complex mechanism of intracellular information
XX transfer. The invention includes a recombinant vector containing a PDE10
XX gene, and a cell transformed with the vector. Sequences AAA09593-A09606

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CC represent PCR primers used in the isolation of the PDE10 polynucleotide
CC sequences of the invention
XX
SQ Sequence 794 AA;
XX
Query Match 98.0%; Score 4123; DB 3; Length 794;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy      1 MEDGSSNNAACFRRLTEGFLSPSLTDEKVAKYLSTHPQVLDFEVSASAEVEMKLRX 60
Db      1 MEDGSSNNAACFRRLTEGFLSPSLTDEKVAKYLSTHPQVLDFEVSASAEVEMKLRX 60
Qy      61 TNKADBPSPKSVSYOOPDNNQGVYELNSYIEORLDTGDNHLLLYELSSIIIRATYAD 120
Db      61 TNKADBPSPKSVSYOOPDNNQGVYELNSYIEORLDTGDNHLLLYELSSIIIRATYAD 120
Qy      61 NKKADESPPEKSVSYOOPDNNQGVYELNSYIEORLDTGDNHLLLYELSSIIIRATYAD 120
Db      61 NKKADESPPEKSVSYOOPDNNQGVYELNSYIEORLDTGDNHLLLYELSSIIIRATYAD 120
Qy      121 GFALYFLGECNNNSLCVFIPPGMKEGQPRIPAGPIITGGTTISAVYAKSKRTLLVEDIIGD 180
Db      121 GFALYFLGECNNNSLCVFIPPGMKEGQPRIPAGPIITGGTTISAVYAKSKRTLLVEDIIGD 180
Qy      181 ERFPGGTGLESSTRIQSVYICLPITVAIGDLIGILELYRHWGEARCLSHQEVATNLAWA 240
Db      181 ERFPGGTGLESSTRIQSVYICLPITVAIGDLIGILELYRHWGEARCLSHQEVATNLAWA 240
Qy      181 ERFPGGTGLESSTRIQSVYICLPITVAIGDLIGILELYRHWGEARCLSHQEVATNLAWA 240
Db      181 ERFPGGTGLESSTRIQSVYICLPITVAIGDLIGILELYRHWGEARCLSHQEVATNLAWA 240
Qy      241 SVAIHQVQCRGLAKOTELNDELIVSKYEPDNIYAIDSLHEIMIYAKNLVNADECALF 300
Db      241 SVAIHQVQCRGLAKOTELNDELIVSKYEPDNIYAIDSLHEIMIYAKNLVNADECALF 300
Qy      241 SVAIHQVQCRGLAKOTELNDELIVSKYEPDNIYAIDSLHEIMIYAKNLVNADECALF 300
Db      241 SVAIHQVQCRGLAKOTELNDELIVSKYEPDNIYAIDSLHEIMIYAKNLVNADECALF 300
Qy      301 QVDHKNKELYSDFIGEEKSGPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYADP 360
Db      301 QVDHKNKELYSDFIGEEKSGPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYADP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSGVIGVQMNKISGSAFSGKTDENNFMFAVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSGVIGVQMNKISGSAFSGKTDENNFMFAVFCAL 420
Qy      421 ALHCANMTHRIHSECTIYRVMEKLSYHSICTSEEWQGLMRNLPARICRDIELFFPDIG 480
Db      421 ALHCANMTHRIHSECTIYRVMEKLSYHSICTSEEWQGLMRNLPARICRDIELFFPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRRVRYNNMKAAVVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRRVRYNNMKAAVVAHCMYAI 540
Qy      541 LQNNNGLPFTDLERKGLIACLDHLDHGRFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Db      541 LQNNNGLPFTDLERKGLIACLDHLDHGRFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Qy      601 SILOEGHNIFFSTLSSEYEYQVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Db      601 SILOEGHNIFFSTLSSEYEYQVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Qy      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXD 720
Db      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXD 720
Qy      721 EYPOGQLGFYNAVAIPCYTTLTQILPTEPPLKACADNINQWEKVI RGETAMWISGPGP 780
Db      721 EYPOGQLGFYNAVAIPCYTTLTQILPTEPPLKACADNINQWEKVI RGETAMWISGPGP 780
Qy      781 APSKSTPEKLANVKVED 796
Db      779 ATSKSTSEKPTRKVD 794

RESULT 4
ADT92235
ID ADT92235 standard; protein; 794 AA.
XX
AC ADT92235;
XX
DT 13-JAN-2005 (first entry)

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XX Rat PDE10A2 isoform sequence.  
 XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;  
 XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A2; rat.  
 XX Rattus norvegicus.  
 XX WO2004090126-A2.  
 XX 21-OCT-2004.  
 XX 30-MAR-2004; 2004MO-US009878.  
 XX 03-APR-2003; 2003US-0459603P.  
 XX (MEMO-) MEMORY PHARM CORP.  
 XX Wang D, Bugaj-Gaweda B;  
 XX WPI; 2004-748763/73.  
 XX New isolated polynucleotide comprising a polynucleotide sequence coding  
 XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for  
 XX treating or preventing memory, psychiatric or cognitive disorders.  
 XX Disclosure; SEQ ID NO 20; 93pp; English.  
 XX  
 XX The invention relates polynucleotide sequences coding for mammalian  
 XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for  
 XX identifying an agent that modulates the expression or activity of a  
 XX phosphodiesterase in transfected host cells is provided which involves  
 XX measuring amounts of cAMP or cGMP produced in the presence of the agent.  
 XX The agent inhibits the expression or activity of the phosphodiesterase.  
 XX The polynucleotides are useful in diagnostic assays and for screening  
 XX modulators, specifically inhibitors of PDE10A7. They are also useful for  
 XX treating or preventing memory, psychiatric or cognitive disorders.  
 XX Sequences AD792232-AD792238 represent various mammalian PDE10A isoforms  
 XX used in a comparison study with the murine and rat PDE10A7 sequences.  
 XX  
 XX Sequence 794 AA;  
 XX  
 XX Query Match 98.0%; Score 4123; DB 8; Length 794;  
 XX Best Local Similarity 98.4%; Pred No. 0;  
 XX Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;  
 XX  
 XX 1 MEDGSPNNASCFRRLTGECFLSPSLTDEKVKAYLSLHPQVLDFFVSEVSAAETVEKMLKK 60  
 XX 1 MEDGSPNNASCFRRLTGECFLSPSLTDEKVKAYLSLHPQVLDFFVSEVSAAETVEKMLKK 60  
 XX 61 TNKADDESPKESVRYODTNMGVYELNSYEQRLDTGSDNHLLEYLSITRIATAD 120  
 XX 61 TNKADDESPKESVRYODTNMGVYELNSYEQRLDTGSDNHLLEYLSITRIATAD 120  
 XX 61 NNKADDESPKESVRYODTNMGVYELNSYEQRLDTGSDNHLLEYLSITRIATAD 120  
 XX 121 GPALYFLGECNNSLCVFTIPPGMKEGOPRLIPAGPTTGGTTISAVYAKSKRTLLVEDILGD 180  
 XX 121 GPALYFLGECNNSLCVFTIPPGMKEGOPRLIPAGPTTGGTTISAVYAKSKRTLLVEDILGD 180  
 XX 121 GPALYFLGECNNSLCVFTIPPGMKEGOPRLIPAGPTTGGTTISAVYAKSKRTLLVEDILGD 180  
 XX 181 BRPFGTGLGSGTRIQSVLCPIVTAIGDLIGILEYRHMGEAKCLSHQEVATNLAWA 240  
 XX 181 BRPFGTGLGSGTRIQSVLCPIVTAIGDLIGILEYRHMGEAKCLSHQEVATNLAWA 240  
 XX 181 BRPFGTGLGSGTRIQSVLCPIVTAIGDLIGILEYRHMGEAKCLSHQEVATNLAWA 240  
 XX 241 SVAIHQOVQCRGLAQOTELNDLFLVSKTYFPNIVAIISLHIMITYANLVNARCLAF 300  
 XX 241 SVAIHQOVQCRGLAQOTELNDLFLVSKTYFPNIVAIISLHIMITYANLVNARCLAF 300  
 XX 241 SVAIHQOVQCRGLAQOTELNDLFLVSKTYFPNIVAIISLHIMITYANLVNARCLAF 300  
 XX 301 QVDHKNKELYSPLPIGEEKKEKPIFKKTKEIRFSIEKGIAGOVARTGVNLIPAYADP 360  
 XX 301 QVDHKNKELYSPLPIGEEKKEKPIFKKTKEIRFSIEKGIAGOVARTGVNLIPAYADP 360  
 XX 301 QVDHKNKELYSPLPIGEEKKEKPIFKKTKEIRFSIEKGIAGOVARTGVNLIPAYADP 360  
 XX 361 RPNREVDLYTGTNTNIIICMPIVSRGSLGVGVQVNNKISGSAFSKTDENNFMFAVFCAL 420  
 XX 361 RPNREVDLYTGTNTNIIICMPIVSRGSLGVGVQVNNKISGSAFSKTDENNFMFAVFCAL 420

QY 421 ALHCANMYRIRHSSECIYRYTMEKLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIG 480  
 DB 421 ALHCANMYRIRHSSECIYRYTMEKLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIG 480  
 QY 481 PFENMMPGIFVYMIHRSCTGSCFELEKLCRFIMSVKKNRYRVPYNNWKAATVAHCAI 540  
 DB 481 PFENMMPGIFVYMIHRSCTGSCFELEKLCRFIMSVKKNRYRVPYNNWKAATVAHCAI 540  
 QY 541 LONNNGFLTDLERGLLACCHDLDRGFNSYLOKFDHPLAALYSTNEOHHSQTV 600  
 DB 541 LONNNGFLTDLERGLLACCHDLDRGFNSYLOKFDHPLAALYSTNEOHHSQTV 600  
 QY 601 SILOEGNIFSTLSSSEYEQVLEIRKAIATDIALYFGRKOLEMYQTSINLHNS 660  
 DB 601 SILOEGNIFSTLSSSEYEQVLEIRKAIATDIALYFGRKOLEMYQTSINLHNS 660  
 QY 661 HRDRIYGLMNTACDLCVYTKLMPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720  
 DB 661 HRDRIYGLMNTACDLCVYTKLMPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720  
 QY 721 EYPOGQLAFYNAVAIPCTTTLTQILPTEPILKACRDNLNOMEKVIIRGEETAMTISGSP 780  
 DB 721 EYPOGQLAFYNAVAIPCTTTLTQILPTEPILKACRDNLNOMEKVIIRGEETAMTIS--GP 778  
 QY 781 APSKSTPEKLNKVED 796  
 DB 779 ATSKSTSEKPTRKVD 794  
 XX  
 XX RESULT 5  
 XX AD792238  
 XX ID AD792238 standard; protein; 779 AA.  
 XX  
 XX AD792238;  
 XX  
 XX 13-JAN-2005 (first entry)  
 XX  
 XX Mouse PDE10A-b isoform sequence.  
 XX  
 XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;  
 XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A-b; mouse.  
 XX Mus musculus.  
 XX WO2004090126-A2.  
 XX 21-OCT-2004.  
 XX 30-MAR-2004; 2004MO-US009878.  
 XX 03-APR-2003; 2003US-0459603P.  
 XX (MEMO-) MEMORY PHARM CORP.  
 XX Wang D, Bugaj-Gaweda B;  
 XX WPI; 2004-748763/73.  
 XX New isolated polynucleotide comprising a polynucleotide sequence coding  
 XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for  
 XX treating or preventing memory, psychiatric or cognitive disorders.  
 XX Disclosure; SEQ ID NO 23; 93pp; English.  
 XX  
 XX The invention relates polynucleotide sequences coding for mammalian  
 XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for  
 XX identifying an agent that modulates the expression or activity of a  
 XX phosphodiesterase in transfected host cells is provided which involves  
 XX measuring amounts of cAMP or cGMP produced in the presence of the agent.  
 XX The agent inhibits the expression or activity of the phosphodiesterase.  
 XX The polynucleotides are useful in diagnostic assays and for screening  
 XX modulators, specifically inhibitors of PDE10A7. They are also useful for

treating or preventing memory, psychiatric or cognitive disorders.  
 CC Sequences ADT92217-ADT92218 represent various mammalian PDE10A isoforms  
 CC used in a comparison study with the murine and rat PDE10A7 sequences.

Sequence 779 AA;

Query Match 97.0%; Score 4080; DB 8; Length 779;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LTDEKAVATLSLHPQVLDSESVSAETVEKMLKRTKAKADESPKESVRYODTNMGG 83  
 DB 7 LTDEKAVATLSLHPQVLDSESVSAETVEKMLKRTKAKADESPKESVRYODTNMGG 66  
 QY 84 VYVELNSYIEORLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVIPPMK 143  
 DB 67 VYVELNSYIEORLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVIPPMK 126  
 QY 144 EGOPLIPAGPTTGGTTISAVAKSRKTLVEDILDEPRPGTGLESTRIQSVCLPI 203  
 DB 127 EGOPLIPAGPTTGGTTISAVAKSRKTLVEDILDEPRPGTGLESTRIQSVCLPI 186  
 QY 204 VTAIGDLIGILELYRMGKBAFCLSHQEVATNLAWSVAIHQVOYCRGLAKOTELNDEL 263  
 DB 187 VTAIGDLIGILELYRMGKBAFCLSHQEVATNLAWSVAIHQVOYCRGLAKOTELNDEL 246  
 QY 264 LDVSKTYFDNIVALDLSLHIMIYAKNLVNAADRCALFOVDHKNKELYSDFDIEKEKG 323  
 DB 247 LDVSKTYFDNIVALDLSLHIMIYAKNLVNAADRCALFOVDHKNKELYSDFDIEKEKG 306  
 QY 324 PIPKTKETIRFSIEKGIAGQVARTGVLNPDAYADPRFREVDLYGTGYYTRNIIICMPY 383  
 DB 307 PIPKTKETIRFSIEKGIAGQVARTGVLNPDAYADPRFREVDLYGTGYYTRNIIICMPY 366  
 QY 384 SSGSVIGVQVMWVKISGSAFSTKDENNPKMAFVALHLCAMMYRIRHSECIYATWE 443  
 DB 367 SSGSVIGVQVMWVKISGSAFSTKDENNPKMAFVALHLCAMMYRIRHSECIYATWE 426  
 QY 444 KLSYHSICTSEEWQGLMRPNLPARICRDIELFFHFDIGPEENMWPGLFVYMIHRSCTGSCF 503  
 DB 427 KLSYHSICTSEEWQGLMRPNLPARICRDIELFFHFDIGPEENMWPGLFVYMIHRSCTGSCF 486  
 QY 504 ELEKLCRFIVSVKKNRYRVPYHNWKIAVTVAHCMYAILQNNNGLFIDLERKGLIICLCH 563  
 DB 487 ELEKLCRFIVSVKKNRYRVPYHNWKIAVTVAHCMYAILQNNNGLFIDLERKGLIICLCH 546  
 QY 564 DLDRHGPSNSYLQKTFHPLAALYSTTMEQHFSQTVSIIQLGSHNIFSTLSSSEYQVL 623  
 DB 547 DLDRHGPSNSYLQKTFHPLAALYSTTMEQHFSQTVSIIQLGSHNIFSTLSSSEYQVL 606  
 QY 624 EILIRKAIATDLDLALYFGRKQLEBMYOTGSLNHNOSHRDVIGLMMTACDLSVTKLMP 683  
 DB 607 EILIRKAIATDLDLALYFGRKQLEBMYOTGSLNHNOSHRDVIGLMMTACDLSVTKLMP 666  
 QY 684 VTKLTANDIYAEFMAEGDEMKKLGIOPIPMWDRDKDEVPQGLGFYNAVAIPCYTTLTQ 743  
 DB 667 VTKLTANDIYAEFMAEGDEMKKLGIOPIPMWDRDKDEVPQGLGFYNAVAIPCYTTLTQ 726  
 QY 744 ILTPTEPLAKCDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLVNVED 796  
 DB 727 ILTPTEPLAKCDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLVNVED 779

RESULT 6

ADT92217 standard; protein; 797 AA.

ADT92217;

13-JAN-2005 (first entry)

Murine phosphodiesterase 10A7 (PDE10A7).

PDE10A7, phosphodiesterase 10A7; phosphodiesterase; nootropic;  
 KW neuroprotective; gene therapy; transgenic; mouse; enzyme.

Mus musculus.

WO2004090126-A2.

21-OCT-2004.

30-MAR-2004; 2004WO-US009878.

03-APR-2003; 2003US-0459603P.

(MEMO-) MEMORY PHARM CORP.

Wang D, Bugaj-Gaweda B;

WPI; 2004-748763/73.

N-PSDB; ADT92216.

New isolated polynucleotide comprising a polynucleotide sequence coding  
 PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for  
 PS creating or preventing memory, psychiatric or cognitive disorders.

Claim 2; SEQ ID NO 2; 93pp; English.

The invention relates polynucleotide sequences coding for mammalian  
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for  
 CC identifying an agent that modulates the expression or activity of a  
 CC phosphodiesterase in transfected host cells is provided which involves  
 CC measuring amounts of cAMP or cGMP produced in the presence of the agent.  
 CC The agent inhibits the expression or activity of the phosphodiesterase.  
 CC The polynucleotides are useful in diagnostic assays and for screening for  
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for  
 CC creating or preventing memory, psychiatric or cognitive disorders. The  
 CC present sequence represents a mouse PDE10A7 enzyme.

Sequence 797 AA;

Query Match 97.0%; Score 4078.5; DB 8; Length 797;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 776; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

QY 12 FRLTECFSPS-----LTDEKAVATLSLHPQVLDSESVSAETVEKMLKRTNKA 64  
 DB 6 FQQAQLCFGRPPSPSATTOGLTDEKAVATLSLHPQVLDSESVSAETVEKMLKRTNKA 65  
 QY 65 KQESPKEVSRVODTNMGGVYVELNSYIEORLDTGDNHLLLYELSSIRIATKADGAL 124  
 DB 66 KQESPKEVSRVODTNMGGVYVELNSYIEORLDTGDNHLLLYELSSIRIATKADGAL 125  
 QY 125 YFLGECNNSLCVFIPPGMEGPRLLPAGPTTGGTTISAVAKSRKTLVEDILGDERPF 184  
 DB 126 YFLGECNNSLCVFIPPGMEGPRLLPAGPTTGGTTISAVAKSRKTLVEDILGDERPF 185  
 QY 185 RGTGLSEGRISQVCLPIYTAIGDLIGILELYRMGKBAFCLSHQEVATNLAWSVAI 244  
 DB 186 RGTGLSEGRISQVCLPIYTAIGDLIGILELYRMGKBAFCLSHQEVATNLAWSVAI 245  
 QY 245 HQVOYCRGLAKQTELDNDELFDLDSKTYFDNIVALDLSLHIMIYAKNLVNAADRCALFOVDH 304  
 DB 246 HQVOYCRGLAKQTELDNDELFDLDSKTYFDNIVALDLSLHIMIYAKNLVNAADRCALFOVDH 305  
 QY 305 KXKELYSDFDIEKEKEGKPIFKTKETIRFSIEKGIAGQVARTGVLNIPDAYADPRFNR 364  
 DB 306 KXKELYSDFDIEKEKEGKPIFKTKETIRFSIEKGIAGQVARTGVLNIPDAYADPRFNR 365  
 QY 365 EVDLYGTGYYTRNIIICMPYISRGSVIGVQVMWVKISGSAFSTKDENNPKMAFVALHLC 424  
 DB 366 EVDLYGTGYYTRNIIICMPYISRGSVIGVQVMWVKISGSAFSTKDENNPKMAFVALHLC 425  
 QY 425 ANMYHRIHSECIYATWELSYHSICTSEEWQGLMRPNLPARICRDIELFFHFDIGPFEN 484

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Db 426 ANMYRIRHSECIYRVMTMEKLSYHSICTSEWQGLMRPNLPARI CRDIELFHFDIGPFEN 485
QY 445 MWPGIFVYVMIHSSCGTSCEPELEKCRFTMSYKKNRRVYVYHMKAVYVAHCMYALLONN 544
Db 446 MWPGIFVYVMIHSSCGTSCEPELEKCRFTMSYKKNRRVYVYHMKAVYVAHCMYALLONN 545
QY 545 NGLFPLDERKGLLIACLDHGRGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTVSILO 604
Db 546 NGLFPLDERKGLLIACLDHGRGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTVSILO 605
QY 605 LEGHNIPTSLSSSEYEQVEIIRKAIITADLALYFGNRKQLEBMYQTGSLNLNOSHRRD 664
Db 606 LEGHNIPTSLSSSEYEQVEIIRKAIITADLALYFGNRKQLEBMYQTGSLNLNOSHRRD 665
QY 665 VTGLMWTACDLSYVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDSDKDEVPQ 724
Db 666 VTGLMWTACDLSYVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDSDKDEVPQ 725
QY 725 GOLGFYNAVAIPCYTTLTQILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSK 784
Db 726 GOLGFYNAVAIPCYTTLTQILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSK 785
QY 785 STPEKLANVKVED 796
Db 786 STPEKLANVKVD 797

RESULT 7
ADT92236
ID ADT92236 standard; protein; 790 AA.
XX ADT92236;
XX 13-JAN-2005 (first entry)
XX Mouse PDE10A3 isoform sequence.
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A3; mouse.
XX Mus musculus.
XX WO2004090126-A2.
XX 21-OCT-2004.
XX 30-MAR-2004; 2004WO-US009878.
XX 03-APR-2003; 2003US-0459603P.
XX (MEMO-) MEMORY PHARM CORP.
XX Wang D, Bugaj-Gaweda B;
XX WPI; 2004-748763/73.
XX New isolated polynucleotide comprising a polynucleotide sequence coding
XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Disclosure; SEQ ID NO 21; 93pp; English.
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms
XX used in a comparison study with the murine and rat PDE10A7 sequences.

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XX SQ Sequence 790 AA;
XX Query Match 96.8%; Score 4072; DB 8; Length 790;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 772; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 24 LTDEKVAKYLALHPVDLDFPSESVSAETVEKMLRKTKNAKDEPSPKVSRVYQDTNNQ 83
Db 18 LTDEKVAKYLALHPVDLDFPSESVSAETVEKMLRKTKNAKDEPSPKVSRVYQDTNNQ 77
QY 84 VYELNSYIEORLDTGDNHLLLYELSSIIRIATVADGALYFLGECNNSLCVFIPEGMK 143
Db 78 VYELNSYIEORLDTGDNHLLLYELSSIIRIATVADGALYFLGECNNSLCVFIPEGMK 137
QY 144 EGQPLRIAGSPITQGTTSAYVAASKRLLVEDILGDRFRFRGCLSEGTPIQSULCPI 203
Db 138 EGQPLRIAGSPITQGTTSAYVAASKRLLVEDILGDRFRFRGCLSEGTPIQSULCPI 197
QY 204 VTAIGDLIGIELYRHWGKEAFCLSHQEVATANLMAASVALHOVQVCRGLAKQTELANDFL 263
Db 198 VTAIGDLIGIELYRHWGKEAFCLSHQEVATANLMAASVALHOVQVCRGLAKQTELANDFL 257
QY 264 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNADRCALFQVDHKNKELYSDFDIGEKEGK 323
Db 258 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNADRCALFQVDHKNKELYSDFDIGEKEGK 317
QY 324 PIFPKTKETIRRSIEKINGIAGVARTGEVNTIPDAVADPFENNEVULYGYTTRNLICMPIV 383
Db 318 PIFPKTKETIRRSIEKINGIAGVARTGEVNTIPDAVADPFENNEVULYGYTTRNLICMPIV 377
QY 384 SRGSVIGVQVQWVKIKSGSAFSKTDENNPKMPAVFCALALHCANNMYRIRHSECIYRVME 443
Db 378 SRGSVIGVQVQWVKIKSGSAFSKTDENNPKMPAVFCALALHCANNMYRIRHSECIYRVME 437
QY 444 KLSYHSICTSEWQGLMRPNLPARI CRDIELFHFDIGPFENMWPGIFVYVMIHRSCTSCF 503
Db 438 KLSYHSICTSEWQGLMRPNLPARI CRDIELFHFDIGPFENMWPGIFVYVMIHRSCTSCF 497
QY 504 ELEKLCRTIMSVKKNRRVPPHNMKHAVTVAHCMYALLONNGLFTDLERKGLLIACLC 563
Db 498 ELEKLCRTIMSVKKNRRVPPHNMKHAVTVAHCMYALLONNGLFTDLERKGLLIACLC 557
QY 564 DLDHRGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTVSILOLEGHNIPTSLSSSEYEQVL 623
Db 558 DLDHRGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTVSILOLEGHNIPTSLSSSEYEQVL 617
QY 624 EIRKAIITADLALYFGNRKQLEBMYQTGSLNLNOSHRRDVI GLMWTACDLSVTKLMP 683
Db 618 EIRKAIITADLALYFGNRKQLEBMYQTGSLNLNOSHRRDVI GLMWTACDLSVTKLMP 677
QY 684 VTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDXRDEVPQGLGFYNAVAIPCTYTLTQ 743
Db 678 VTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDXRDEVPQGLGFYNAVAIPCTYTLTQ 737
QY 744 ILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSKSTPEKLANVKVED 796
Db 738 ILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSKSTPEKLANVKVED 790

RESULT 8
ADT92219
ID ADT92219 standard; protein; 795 AA.
XX ADT92219;
XX 13-JAN-2005 (first entry)
XX Rat phosphodiesterase 10A7 (PDE10A7).
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
XX neuroprotective; gene therapy; transgenic; rat; enzyme.

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OS	Rattus norvegicus.
XX	PN WO2004090126-A2.
XX	PD 21-OCT-2004.
XX	PF 30-MAR-2004; 2004WO-US009878.
XX	PR 03-APR-2003; 2003US-0459603P.
XX	PA (MEMO-) MEMORY PHARM CORP.
XX	PI Wang D, Bugaj-Gaweda B;
XX	DR WPI; 2004-748763/73.
XX	N-PSDB; ADT92218.
PT	New isolated polynucleotide comprising a polynucleotide sequence coding for a mammalian phosphodiesterase 10A7, or its mutation, useful for treating or preventing memory, psychiatric or cognitive disorders.
XX	Claim 3; SEQ ID NO 4; 93pp; English.
CC	The invention relates polynucleotide sequences coding for mammalian phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for identifying an agent that modulates the expression or activity of a phosphodiesterase in transfected host cells is provided which involves measuring amounts of cAMP or GMP produced in the presence of the agent. The agent inhibits the expression or activity of the phosphodiesterase. The polynucleotides are useful in diagnostic assays and for screening modulators, specifically inhibitors of PDE10A7. They are also useful for treating or preventing memory, psychiatric or cognitive disorders. The present sequence represents a rat PDE10A7 enzyme.
SQ	Sequence 795 AA;
Query Match	95.4%; Score 4012.5; DB 8; Length 795;
Best Local Similarity	96.7%; Pred. No. Of
Matches 767; Conservative	5; Mismatches 12; Indels 9; Gaps 3;
DG	11 CRRRLTEC--ELSPS-----LTDEKVAAYLSLHPVLDFEVSSESVSAETVEKLKRKTNK 63 :: ::
OY	5 CFQQQLCRGPSSANTRGTLDEKVAAYLSLHPVLDLPFSESASATVEKMKLRKNKK 64
DG	64 AKDSEPKEVSRYODTNNGGVVELNSYIEORLDTGDGNHLLLYELSIIIRIATYADGA 123 : :
OY	65 AEDESPPEVSRYODTNNGVVVELNSYIEORLDTGDGNHLLLYELSIIRIATYADGFA 124
OY	124 LYFLGECNNSLCVFPFGMEKGQPPLIPAGPTTGTTISAVYAKSRKTLVEDIDGERRF 183
DG	125 LYFLGECSNNSLCFVTPPGMEKGQPLIPAGPTTGTTISAVYAKSRKTLVEDIDGERRF 184
OY	184 PRGTLESGTRIOSYLCLPIYAIGDLGIILELYHWMGKAFCISHOEVAATANLAMASVA 243 
DG	185 PRGTLESBSTRIOSQLCLPIYAIGDLGIILELYHWMGKAFCISHOEVAATANLAMASVA 244
OY	244 IHQVVCRCGLAQOTELANDFLDVSKTYPPDNIVAIDSLEHHIMIVAKNLVNADRCAALFOVD 303
DG	245 IHQVVCRCGLAQOTELANDFLDVSKTYPPDNIVAIDSLEHHIMIVAKNLVNADRCAALFOVD 304
OY	304 HKNRELSDLPITIGEBKGKPFFKTKTGRIFSEIKGIAGQAVARTGEVINIPRAYADPREFN 363    :
DG	305 HNKNELYSDDLPIIGEBKGKPVFKTKTKEIRFSIEKGIAGQAVARTGEVINIPRAYADPREFN 364
OY	364 REVDLYTGTTNNILCMPIVSRSYGVIQVQWYNKS SGAASFSTKDENRPFMFVPFCALLAH 423 
DG	365 REVDLYTGTTNNILCMPIVSRSYGVIQVQWYNKS SGAASFSTKDENRPFMFVPFCALLAH 424
OY	424 CANMYTHRIHSCEICIRVTWEKLSYHSICTSEEMOGIMRENLPARICRDIELFHFDIGPFE 483
DG	425 CANMYTHRIHSCEICIRVTWEKLSYHSICTSEEMOGIMRENLPARICRDIELFHFDIGPFE 484
OY	484 NMYPGGI FYYMHIRSCGTSCEBELKLCRPMYSVKQNYRRVRPHNMKHAAVTVMCHMTAILON 543

Db	485	NMFGIFVYMIHRS	CGTSCFELEKLCRFIMS	VKKYRVRPYHNWKA	VTVAHCMTAILQN	544
QY	544	NGGIFPTLIERK	GLIIAACLCHDIDH	RGSNSYLQKEDH	PLAALYSTMTSEOH	HSFQTSIL 603
Db	545	NNGIFPTLIERK	GLIIAACLCHDIDH	RGSNSYLQKEDH	PLAALYSTMTSEOH	HSFQTSIL 604
QY	604	QLEGHNIFSTLS	SEYEQVLEIIRK	AIITADLALYFN	RKQLBEMVOTG	SILNINQSHRD 663
Db	605	QLEGHNIFSTLS	SEYEQVLEIIRK	AIITADLALYFN	RKQLBEMVOTG	SILNINQSHRD 664
QY	664	RVIGIMMTACD	LCVTKLMPYTKL	TANDIYAEFMA	BGDEMKLGIGI	OPIMMDRDKRDEVP 723
Db	665	RVIGIMMTACD	LCVTKLMPYTKL	TANDIYAEFMA	BGDEMKLGIGI	OPIMMDRDKRDEVP 724
QY	724	OGQIGFNNAA	IPCYTTLTQILP	PTBELLACRPN	LNQWEKVRGSE	TAMMISGPGAPS 783
Db	725	OGQIGFNNAA	IPCYTTLTQILP	PTBELLACRPN	LNQWEKVRGSE	TAMMISGPGAPS 782
QY	784	KSTPEKLN	VKVED 796			
Db	783	KSTPEKLN	VKVED 795			

RESULT 9

AAB26854

ID AAB26854 standard; protein; 789 AA.

XX AC AAB26854;

XX DT 29-JAN-2001 (first entry)

XX DE Human phosphodiesterase 10 (PDE10) amino acid sequence 2.

XX KM Phosphodiesterase 10; PDE10; human.

XX OS Homo sapiens.

XX FN JP2000224992-A.

PD 15-AUG-2000.

XX PF 11-MAY-1999; 99JP-00129343.

XX FR 30-NOV-1998; 98JP-00338861.

XX PA (TANABE SEIYAKU CO.

DR MPI; 2000-605129/58.

DR N-PSDB; AAA09590.

PT Novel phosphodiesterase and its gene for research on complex mechanism of intracellular information transfer.

PS Disclosure; Page 16-19; 29pp; Japanese.

XX Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)

CC proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful

CC for research on the complex mechanism of intracellular information

CC transfer. The invention includes a recombinant vector containing a PDE10

CC gene, and a cell transformed with the vector. Sequences AAA09593-A09606

CC represent PCR primers used in the isolation of the PDE10 polynucleotide

CC sequences of the invention

XX SQ Sequence 789 AA;

QY Query Match 95.2%; Score 4004; DB 3; Length 789;

Best Local Similarity 95.6%; Pred. No. 0;

Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

1 MEDGSSNNASGFRRLTECFILSPSLTDEKVAKYLISHPQVLDFVSESVSAETVEKMLRK 60

1 MEDGSSNNASGFRRLTECFILSPSLTDEKVAKYLISHPQVLDFVSESVSAETVEKMLRK 60

Qy	61	INXKADSPREVSXYPOTMNOGVVYELNSYIEOQLDTCGDHMLLYELSSIRIATKXD	120
Dp	61	NNKDEBSAPXEVSRXQDTMNOGVVYELNSYIEOQLDTCGDHMLLYELSSIRIATKXD	120
Qy	121	GFALYFLGECNNLSICVPIFPGMKEGQPRLIIPAGPIQCTTISAVYAKSRKTLVEDILD	180
Dp	121	GFALYFLGECNNLSICIFPPRPIKKGKPRLIIPAGPIQCTTISAVYAKSRKTLVEDILD	180
Qy	181	ERFPRGTJESGTRIQSVLCPIVTAIGDLIGILBYLRHWGKEAFCLSHQEVATANLAWA	240
Dp	181	ERFPRGTJESGTRIQSVLCPIVTAIGDLIGILBYLRHWGKEAFCLSHQEVATANLAWA	240
Qy	241	SVALHNOVCGGLAQOTELNDLNDLVSKTYPNINYAIDSLBHEIMYANOLVANDCALF	300
Dp	241	SVALHNOVCGGLAQOTELNDLNDLVSKTYPNINYAIDSLBHEIMYANOLVANDCALF	300
Qy	301	QVDHKNKELYSDFPIGEEKGKPIFKTKKEIRFSIEKIAQVARTGEVLNIPDAVADP	360
Dp	301	QVDHKNKELYSDFPIGEEKGKPPFKTKKEIRFSIEKIAQVARTGEVLNIPDAVADP	360
Qy	361	RFRNREVDLYGTGTTNIIICMPIVSRSQVIGVQVANKISGSAFSGKTENNPKMAVFCAL	420
Dp	361	RFRNREVDLYGTGTTNIIICMPIVSRSQVIGVQVANKISGSAFSGKTENNPKMAVFCAL	420
Qy	421	ALHCAKMTARIRHSCICIRVYMEKLSYSHICISEEKOGLMRPRLPARICRDIETFRHFDIG	480
Dp	421	ALHCAKMTARIRHSCICIRVYMEKLSYSHICISEEKOGLMFTLPVRLKEIELEFRHFDIG	480
Qy	481	PFEKNMPGIFVYMIRHSCGTSCEFELEKLCRFMTSVYKQNRARVYHNMKCAVYVAHCMYAI	540
Dp	481	PFEKNMPGIFVYMIRHSCGTSCEFELEKLCRFMTSVYKQNRARVYHNMKCAVYVAHCMYAI	540
Qy	541	LÖNNNGLEFTDERKGLIACLCHDLDRGFSNSYLOKFDHPLAALYSTSTMEQHHSQTV	600
Dp	541	LÖNNHTLFTDERKGLIACLCHDLDRGFSNSYLOKFDHPLAALYSTSTMEQHHSQTV	600
Qy	601	SILÖLEGNIYSTLSSSEYEOULETIRKAIINTDALYRGNRKÖLEBMVQGSINLHNS	660
Dp	601	SILÖLEGNIYSTLSSSEYEOULETIRKAIINTDALYRGNRKÖLEBMVQGSINLHNS	660
Qy	661	HRDRYIGLMTARACDLSVTKLMPVTKLTANDIYAEFWAGDEKKUGIOPIPMDDKXD	720
Dp	661	HRDRYIGLMTARACDLSVTKLMPVTKLTANDIYAEFWAGDEKKUGIOPIPMDDKXD	720
Qy	721	EVPOGOLGFYNAVAIPCYTTLTQIILPTEPRLKACHDNLQNEKVIIRGEETAMWISGPB	780
Dp	721	EVPOGOLGFYNAVAIPCYTTLTQIILPTEPRLKACHDNLQNEKVIIRGEETATWISSPV	780
Qy	781	APSKSTPE 788	
Dp	781	AQKAASE 788	

PF 30-MAR-2004; 2004MO-US009878.  
 XX  
 PR 03-APR-2003; 2003US-0459603P.  
 XX  
 PA (MEMO-) MEMORY PHARM CORP.  
 XX  
 PI Wang D, Bugaj-Gaweda B;  
 XX  
 DR WPI; 2004-748763/73.  
 XX  
 PT New isolated polynucleotide comprising a polynucleotide sequence coding  
 PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for  
 PT treating or preventing memory, psychiatric or cognitive disorders.  
 XX  
 XX Disclosure; SEQ ID NO 18; 93pp; English.  
 XX  
 XX The invention relates polynucleotide sequences coding for mammalian  
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for  
 CC identifying an agent that modulates the expression or activity of a  
 CC phosphodiesterase in transfected host cells is provided which involves  
 CC measuring amounts of cAMP or cGMP produced in the presence of the agent.  
 CC The agent inhibits the expression or activity of the phosphodiesterase.  
 CC The polynucleotides are useful in diagnostic assays and for screening  
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for  
 CC treating or preventing memory, psychiatric or cognitive disorders.  
 CC Sequences AD792232-AD792238 represent various mammalian PDE10A isoforms  
 CC in a comparison study with the murine and rat PDE10A7 sequences.  
 XX  
 XX Sequence 789 AA;

50	Sequence 789 AA;				
	Query Match	95.2%	Score 4004;	DB 8;	Length 789;
	Best Local Similarity	95.6%	Pred. No. 0;		
	Matches 753; Conservative	19;	Mismatches	16;	Indels 0;
			Gaps		0;

[illegible]



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QY      601  SILEGHNHIFSTLSSSEYEOVLIRKAIITDIALYFGNRKQLEEMVQTSGLNHANS 660
DB      601  SILEGHNHIFSTLSSSEYEOVLIRKAIITDIALYFGNRKQLEEMVQTSGLNHANS 660
QY      661  HDRVYIGLMTACDLCSTYKLPVYTLTANDIYAEFMAEGDEMKKLGIOPIPMRDKXD 720
DB      661  HDRVYIGLMTACDLCSTYKLPVYTLTANDIYAEFMAEGDEMKKLGIOPIPMRDKXD 720
QY      721  EYPOGOLGFYNAVAIPCYTTLTQILPTEPPLAKACRDNLQWEKVI RGEETAMWISGPGP 780
DB      721  EYPOGOLGFYNAVAIPCYTTLTQILPTEPPLAKACRDNLQWEKVI RGEETAMWISGPGP 780
QY      781  APSKSTPE 788
DB      781  AQKAAASE 788

RESULT 11
AAB26856
ID      AAB26856 standard; protein; 788 AA.
XX      AAB26856;
XX      29-JAN-2001 (first entry)
XX      Human phosphodiesterase 10 (PDE10) amino acid sequence 4.
XX      Phosphodiesterase 10; PDE10; human.
XX      Homo sapiens.
XX      JP2000224992-A.
XX      15-AUG-2000.
XX      11-MAY-1999; 99JP-00129343.
XX      PR      30-NOV-1996; 98JP-00338861.
XX      (TANA) TANABE SEIYAKU CO.
XX      WPI; 2000-605129/58.
XX      Novel phosphodiesterase and its gene for research on complex mechanism of
XX      intracellular information transfer.
XX      Disclosure; Page 24-27; 29pp; Japanese.
XX      Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
XX      protein AAB26853-B26856. Phosphodiesterase 10 and its gene are useful
XX      for research on the complex mechanism of intracellular information
XX      transfer. The invention includes a recombinant vector containing a PDE10
XX      gene, and a cell transformed with the vector. Sequences AAA09593-A09606
XX      represent PCR primers used in the isolation of the PDE10 polynucleotide
XX      sequences of the invention
XX      Sequence 788 AA;

Query Match      95.0%; Score 3997; DB 3; Length 788;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 760; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY      24  LTDEKTKAVYSLHPQVLDVFSSVSATTEKWLKRTNKAKDBSPKESRYODTNMGG 83
DB      18  LTDEKTKAVYSLHPQVLDVFSSVSATTEKWLKRTNKAKDBSPKESRYODTNMGG 77
QY      84  VVYEINSYIEQRDLDTGDNHLLYELESSIRIATKADGFALYFLGECNNSLCVFTIPGMK 143
DB      78  VVYEINSYIEQRDLDTGDNHLLYELESSIRIATKADGFALYFLGECNNSLCVFTIPGMK 137
QY      144 EGQPRLLIAGPITGCTTISAVAKSKTLLVEDILGDERFPAGTGLASGTRIQSVLCLEPI 203

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DB      138 EGQPRLLIAGPITGCTTISAVAKSKTLLVEDILGDERFPAGTGLASGTRIQSVLCLEPI 197
QY      204 VTAIGDLIGILELYRHWGKEAFCLSHOVATNTANLMA5AIAHQVQVCGGLAQOTLNDL 263
DB      198 VTAIGDLIGILELYRHWGKEAFCLSHOVATNTANLMA5AIAHQVQVCGGLAQOTLNDL 257
QY      264  LDVSKTYEPDNIYVAIDSLLEHIMIYAKNLVNADRCALFOVDHNGKELYSPLDIGEKEGK 323
DB      258  LDVSKTYEPDNIYVAIDSLLEHIMIYAKNLVNADRCALFOVDHNGKELYSPLDIGEKEGK 317
QY      324  PIFKTKTEIRFSIEKGIAGOVARTGEVLNIPDAVADPRENREVDLYGTGTTNIIICMPIV 383
DB      318  PIFKTKTEIRFSIEKGIAGOVARTGEVLNIPDAVADPRENREVDLYGTGTTNIIICMPIV 377
QY      384  SRGSYIGVQVQVANKISGSAPSKTDENRFKMFVFCALALHCANMTHRIHNSCIRVYME 443
DB      378  SRGSYIGVQVQVANKISGSAPSKTDENRFKMFVFCALALHCANMTHRIHNSCIRVYME 437
QY      444  KLSYHSICTSEEWQGLMRPNLPARI CRDIELFHPDIGPEENM PGI FVYMIRHSCGTSCE 503
DB      438  KLSYHSICTSEEWQGLMRPNLPARI CRDIELFHPDIGPEENM PGI FVYMIRHSCGTSCE 497
QY      504  BLEKLCRFIMSYKQYRVRPYHNMKHAVTVAHCAVAILQNNNGLFTDLERKGLIACLC 563
DB      498  BLEKLCRFIMSYKQYRVRPYHNMKHAVTVAHCAVAILQNNNGLFTDLERKGLIACLC 557
QY      564  DLDHGRFSNSYLOKRDHPALALYSTMEQHHPSQTVSILQLEGNHIFSTLSSSEYEOVL 623
DB      558  DLDHGRFSNSYLOKRDHPALALYSTMEQHHPSQTVSILQLEGNHIFSTLSSSEYEOVL 617
QY      624  EIIIRKAIITDIALYFGNRKQLEEMVQTSGLNLHNOSHRDRIYGLMNTACDLCSTYKLP 683
DB      618  EIIIRKAIITDIALYFGNRKQLEEMVQTSGLNLHNOSHRDRIYGLMNTACDLCSTYKLP 677
QY      684  YTKLTANDIYAEFMAEGDEMKKLGIOPIPMRDKDEVPQOLGFYNAVAIPCYTTLTQ 743
DB      678  YTKLTANDIYAEFMAEGDEMKKLGIOPIPMRDKDEVPQOLGFYNAVAIPCYTTLTQ 737
QY      744  ILPTEPPLKACRDNLQWEKVI RGEETAMWISGPGAPSKTPEKLVAKVED 796
DB      738  ILPTEPPLKACRDNLQWEKVI RGEETAMWIS--GPATSKTSSEKPTRKVD 788

RESULT 12
ADT92237
ID      ADT92237 standard; protein; 788 AA.
XX      ADT92237;
XX      13-JAN-2005 (first entry)
XX      DE      Rat PDE10A3 isoform sequence.
XX      PDE10A7, phosphodiesterase 10A7; phosphodiesterase; nootropic;
XX      neuroprotective; gene therapy; transgenic; enzyme; PDE10A3; rat.
XX      Rattus norvegicus.
XX      PN      WO2004090126-A2.
XX      21-OCT-2004.
XX      30-MAR-2004; 2004WO-US009878.
XX      PR      03-APR-2003; 2003US-0459603P.
XX      (MEMO-) MEMORY PHARM CORP.
XX      Wang D, Bugaj-Gaweda B;
XX      WPI; 2004-748763/73.
XX      New isolated polynucleotide comprising a polynucleotide sequence coding

```

PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for  
 PT treating or preventing memory, psychiatric or cognitive disorders.

PS Disclosure: SEQ ID NO 22; 93pp; English.

CC The invention relates polynucleotide sequences coding for mammalian  
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for  
 CC identifying an agent that modulates the expression or activity of a  
 CC phosphodiesterase in transfected host cells is provided which involves  
 CC measuring amounts of cAMP or cGMP produced in the presence of the agent.  
 CC The agent inhibits the expression or activity of the phosphodiesterase.  
 CC The polynucleotides are useful in diagnostic assays and for screening  
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for  
 CC treating or preventing memory, psychiatric or cognitive disorders.  
 CC Sequences AD792232-AD792238 represent various mammalian PDE10A isoforms  
 CC used in a comparison study with the murine and rat PDE10A7 sequences.

XX Sequence 788 AA;

Query Match 95.0%; Score 3997; DB 8; Length 788;

Best Local Similarity 98.3%; Pred. No. 0; Mismatches 8; Indels 2; Gaps 1;

Matches 760; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

24 LTDEKVKAYLSLHPVLDSESVSAETVEKMLKRTKAKDESPKESRYODTNMG 83  
 18 LTDEKVKAYLSLHPVLDSESVSAETVEKMLKRTKAKDESPKESRYODTNMG 77  
 84 VYELNSTYEQRLDTGGDNHLLYELSSITRIATADGALYFLGECNNSLCVFIPGKK 143  
 78 VYELNSTYEQRLDTGGDNHLLYELSSITRIATADGALYFLGECNNSLCVFIPGKK 137  
 144 EGQPLIPAGPIITGGTISAYVAKSRKTLVEDIDGDERFPFGTGESGTRIQSVLCPI 203  
 138 EGQPLIPAGPIITGGTISAYVAKSRKTLVEDIDGDERFPFGTGESGTRIQSVLCPI 197  
 204 VTAIGDLIGILELYHMGKEAFCLSHOEVAATNLAMASVAIHQVQCRGLAKQTEINDEL 263  
 198 VTAIGDLIGILELYHMGKEAFCLSHOEVAATNLAMASVAIHQVQCRGLAKQTEINDEL 257  
 264 LDVSKTYPDNIYALISLHEIMITYAKNLVNAADRCALFOVDHKKELYSLEFDIGEEKG 323  
 258 LDVSKTYPDNIYALISLHEIMITYAKNLVNAADRCALFOVDHKKELYSLEFDIGEEKG 317  
 324 PIFKTKETIRSEIEKIGIVARTEGVANI PDAVADPRNRREVDLYTGTTNIIICMPIV 383  
 318 PIFKTKETIRSEIEKIGIVARTEGVANI PDAVADPRNRREVDLYTGTTNIIICMPIV 377  
 384 SRGSYIGVQVWNKISGSAFSKTDENNFPMFAVFCALALHCAHMYHRIHSECIYRTME 443  
 378 SRGSYIGVQVWNKISGSAFSKTDENNFPMFAVFCALALHCAHMYHRIHSECIYRTME 437  
 444 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPENNPGIFVYMIRHSCGTSCF 503  
 438 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPENNPGIFVYMIRHSCGTSCF 497  
 504 ELEKICRPTMSYKKNYRRVRYNMMKHAIVVAHCAVAILLONNNGLFTDLERKELALACCH 563  
 498 ELEKICRPTMSYKKNYRRVRYNMMKHAIVVAHCAVAILLONNNGLFTDLERKELALACCH 557  
 564 DLDHGFNSNYLQKDPHLAALYSTSTMEQHHSQTSVILQLEGNHIFSTLSSSEYEQVL 623  
 558 DLDHGFNSNYLQKDPHLAALYSTSTMEQHHSQTSVILQLEGNHIFSTLSSSEYEQVL 617  
 624 EIRRAIATATDALYFGNKKOLEBMYQTSGLNLHNSHRDRIYIGLMTACDLCSTYKMP 683  
 618 EIRRAIATATDALYFGNKKOLEBMYQTSGLNLHNSHRDRIYIGLMTACDLCSTYKMP 677  
 664 VTKLANTIYAEFMAEGEMKGLGIOPIMMDRDRDEVPOGOLGFYNAVALPCYTTLLQ 743  
 678 VTKLANTIYAEFMAEGEMKGLGIOPIMMDRDRDEVPOGOLGFYNAVALPCYTTLLQ 737  
 744 ILPTEPLKACRDNLNQMEKVIKGEETAMWISGCPAPSKSTPEKLNKVED 796

DB 728 ILPTEPLKACRDNLNQMEKVIKGEETAMWIS--GPATSKSTSEKPYRKVD 788

RESULT 13

AA13935

AA13935 standard; protein; 803 AA.

AA13935;

14-JUL-1999 (first entry)

Human phosphodiesterase, PDE8.

Phosphodiesterase 8; PDE8; human; cyclic nucleotide pathway; therapy;

intracellular cyclic nucleotide level modulation; cAMP; cGMP.

Homo sapiens.

WO919495-A1.

22-APR-1999.

16-OCT-1998; 98WO-US021956.

16-OCT-1997; 97US-00951648.

(ICOS-) ICOS CORP.

Loughney K;

WPI; 1999-277645/23.

N-PEDB; AAX36711.

New isolated phosphodiesterase genes and polypeptides for identifying

specific binding partners.

Claim 3; Page 50-55; 80pp; English.

This sequence is the human phosphodiesterase 8 (PDE8) of the invention.

The phosphodiesterase genes and polypeptides are used to develop products

for treating conditions in which cyclic nucleotide pathways are aberrant

and for modulation of intracellular cyclic nucleotide levels. The PDE8

polypeptides exhibit high affinity for hydrolysis of both cAMP and cGMP

but relatively low sensitivity to enzyme inhibitors specific for other

PDE families. The PDE8A polypeptides and polynucleotides can be used for

identifying their specific binding partners. The products can provide

approaches for treating conditions in which cyclic nucleotide pathways

are aberrant as well as conditions in which modulation of intracellular

cAMP and/or cGMP levels in certain cell types is desirable

Sequence 803 AA;

Query Match 95.0%; Score 3997; DB 2; Length 803;

Best Local Similarity 95.4%; Pred. No. 0;

Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

1 MEDGPNNAAGFRRLTEGFLSPSLTDEKVKAYLSLHPVLDSESVSAETVEKMLRK 60

15 MEDGPNNAAGFRRLTEGFLSPSLTDEKVKAYLSLHPVLDSESVSAETVEKMLRK 74

61 TNKADDESPKESRYODTNMGVYELNSTYEQRLDTGGDNHLLYELSSITRIATRAD 120

75 NKSSEDESPKESRYODTNMGVYELNSTYEQRLDTGGDNHLLYELSSITRIATRAD 134

121 GPALYFLGECNNSLCVFIPGKESQPLIPAGPIITGGTISAYVAKSRKTLVEDIDG 180

135 GPALYFLGECNNSLCVFIPGKESQPLIPAGPIITGGTISAYVAKSRKTLVEDIDG 194

181 BRPFGTGESGTRIQSVLCPIYTAGDLIGILELYHMGKEAFCLSHOEVAATNLAMA 240

195 BRPFGTGESGTRIQSVLCPIYTAGDLIGILELYHMGKEAFCLSHOEVAATNLAMA 254

241 SVAIHQVQCRGLAKQTEINDELVDVSKTYPDNIYALISLHEIMITYAKNLVNAADRCALF 300

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Db      |||||
255  SVAIHQVOCRLAQTEINDFLDVSKYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 314
Qy      |||||
301  QVDHKNKELYSDFPIGEKEGKPIFKTKKEIRFSIEKIAQVARTGEVLNIPDAYADP 360
Db      |||||
315  QVDHKNKELYSDFPIGEKEGKPVFKTKKEIRFSIEKIAQVARTGEVLNIPDAYADP 374
Qy      |||||
361  RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 420
Db      |||||
375  RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 434
Qy      |||||
421  ALHCANMTHRIHSECTIYVWMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDGG 480
Db      |||||
435  ALHCANMTHRIHSECTIYVWMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDGG 494
Qy      |||||
491  PENNMWPGIFVYVMHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHGMVYAI 540
Db      |||||
495  PENNMWPGIFVYVMHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHGMVYAI 554
Qy      |||||
541  LQNNNGLFPTDLERKGLIACLCCHDLDRGFSNSYLQKPDHPLAALYSTSTMEQHHSQTV 600
Db      |||||
555  LQNNHTLFTDLERKGLIACLCCHDLDRGFSNSYLQKPDHPLAALYSTSTMEQHHSQTV 614
Qy      |||||
601  SILOEGHNIFFSTLSSEYEOVLEIRKAIITADLALYGNRKQLEEMQTSGLNLHNS 660
Db      |||||
615  SILOEGHNIFFSTLSSEYEOVLEIRKAIITADLALYGNRKQLEEMQTSGLNLHNS 674
Qy      |||||
661  HDRVIGLMMTACDLCSTVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720
Db      |||||
675  HDRVIGLMMTACDLCSTVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 734
Qy      |||||
721  EYPOGQLGYNAVAIFCYTTLTQILPTEPPLKACRDNINQWEKVRGSETAMWISGPGP 780
Db      |||||
735  EYPOGQLGYNAVAIFCYTTLTQILPTEPPLKACRDNINQWEKVRGSETAMWISGPGP 794
Qy      |||||
781  APSKSTPE 788
Db      |||||
795  AQAQAASE 802

RESULT 14
AAB28257 standard; protein; 803 AA.
XX      AAB28257;
AC      13-FEB-2001 (first entry)
DT      Human phosphodiesterase 8A1 PDB8A1.
DE      Human phosphodiesterase 8A1; chromosome 6p26-27.
XX      Homo sapiens.
OS      US6133007-A.
XX      US6133007-A.
XX      17-OCT-2000.
XX      PD      16-OCT-1998; 98US-00174437.
XX      PF      16-OCT-1997; 97US-00951648.
XX      PR      16-OCT-1997; 97US-00951648.
XX      PA      (ICOS-) ICOS CORP.
XX      PI      Loughney K;
XX      PT      MPI; 2001-006138/01.
XX      DR      N-PSDB; AAC63696.
XX      New phosphodiesterase 8A (PDB8A) polypeptides useful in the
XX      PT      systematic analysis of the structure and function of PDB8, and for
XX      PT      identifying molecules with which PDB8A will interact.

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PS      Claim 2; Col 39-44; 37pp; English.
XX      The present sequence is human phosphodiesterase 8A1 (PDB8A1).
CC      Phosphodiesterases hydrolyse 3', 5' cyclic nucleotides to their
CC      respective nucleoside 5' monophosphates. The present sequence is a splice
CC      variant of PDB8 (AAB28256). This sequence may be used in the systematic
CC      analysis of the structure and function of PDB8, and for the
CC      identification of molecules with which PDB8 will interact. The coding
CC      sequence for the present protein may be used in hybridisation assays to
CC      detect the capacity of cells to express PDB8, and as a basis for
CC      diagnostic methods useful for identifying a genetic alteration in a PDB8
CC      locus that underlies a disease state or states. The human PDB8 gene has
CC      been localised to chromosome 6p26-27
XX      Sequence 803 AA;
SQ
Query Match      95.0%; Score 3997; DB 4; Length 803;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
Qy      1 MEDGSSNASCRRRLTECFSLSPSLTDEKVKAYLSLHPQVLDFFVESVSAETVEKWKRK 60
Db      15 MEDGSSNASCRRRLTECFSLSPSLTDEKVKAYLSLHPQVLDFFVESVSAETVEKWKRK 74
Qy      61 TYKADDESPKESVRYODTNQGVYELNSYTEORLDGTGSDHLLLELSSTIIRIATKAD 120
Db      75 NKKSDESPKESVRYODTNQGVYELNSYTEORLDGTGSDHLLLELSSTIIRIATKAD 134
Qy      121 GPALYFLGECNNSLCVPIPPGKMEGQPRILPAGPIITGGTTSAYVAKSRKTLVVEDIIGD 180
Db      135 GPALYFLGECNNSLCVPIPPGKMEGQPRILPAGPIITGGTTSAYVAKSRKTLVVEDIIGD 194
Qy      181 ERFPRGTGIESGTRIQSVICLPITVAIGDLIGILBYLHNMWKAACLSHQEVAITNLMAA 240
Db      195 ERFPRGTGIESGTRIQSVICLPITVAIGDLIGILBYLHNMWKAACLSHQEVAITNLMAA 254
Qy      241 SVAIHQVOCRLAQTEINDFLDVSKYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 300
Db      255 SVAIHQVOCRLAQTEINDFLDVSKYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 314
Qy      301 QVDHKNKELYSDFPIGEKEGKPIFKTKKEIRFSIEKIAQVARTGEVLNIPDAYADP 360
Db      315 QVDHKNKELYSDFPIGEKEGKPVFKTKKEIRFSIEKIAQVARTGEVLNIPDAYADP 374
Qy      361 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 420
Db      375 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 434
Qy      421 ALHCANMTHRIHSECTIYVWMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDGG 480
Db      435 ALHCANMTHRIHSECTIYVWMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDGG 494
Qy      481 PENNMWPGIFVYVMHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHGMVYAI 540
Db      495 PENNMWPGIFVYVMHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHGMVYAI 554
Qy      541 LQNNNGLFPTDLERKGLIACLCCHDLDRGFSNSYLQKPDHPLAALYSTSTMEQHHSQTV 600
Db      555 LQNNHTLFTDLERKGLIACLCCHDLDRGFSNSYLQKPDHPLAALYSTSTMEQHHSQTV 614
Qy      601 SILOEGHNIFFSTLSSEYEOVLEIRKAIITADLALYGNRKQLEEMQTSGLNLHNS 660
Db      615 SILOEGHNIFFSTLSSEYEOVLEIRKAIITADLALYGNRKQLEEMQTSGLNLHNS 674
Qy      661 HDRVIGLMMTACDLCSTVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720
Db      675 HDRVIGLMMTACDLCSTVKLMPVTGLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 734
Qy      721 EYPOGQLGYNAVAIFCYTTLTQILPTEPPLKACRDNINQWEKVRGSETAMWISGPGP 780
Db      735 EYPOGQLGYNAVAIFCYTTLTQILPTEPPLKACRDNINQWEKVRGSETAMWISGPGP 794
Qy      781 APSKSTPE 788

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Db 795 AQAASE 802

RESULT 15  
AAE39535  
AAE39535 standard; protein; 803 AA.  
XX AAE39535;  
XX AAE39535;  
DT 18-DEC-2003 (first entry)  
XX Human phosphodiesterase 8 (PDE8) A2 splice variant, PB66a.  
DE Human phosphodiesterase 8; PDE8; human; enzyme.  
KM Phosphodiesterase 8; PDE8; human; enzyme.  
XX Homo sapiens.  
XX US656087-B1.  
PN 20-MAY-2003.  
PD 11-OCT-2000; 2000US-00686055.  
XX 16-OCT-1997; 97US-00951648.  
XX 16-OCT-1998; 98US-00174437.  
XX (ICOS-) ICOS CORP.  
XX Loughney K;  
XX MPI; 2003-719642/68.  
DR N-PSDB; AAD59989.  
XX Identifying a specific binding partner of phosphodiesterase 8 (PDE8)  
PT useful for purifying PDE8 products in fluid samples comprises contacting  
PT PDE8 with a compound and detecting binding.  
XX Claim 1; Col 39-44; 37pp; English.  
XX The invention relates to a method for identifying a specific binding  
CC partner of phosphodiesterase 8 (PDE8). The method is useful for  
CC identifying a specific binding partner of PDE8, which inhibits or  
CC enhances activity of PDE8. The binding partners of PDE8 are useful for  
CC purification, detection or quantification of PDE8 products in fluid and  
CC tissue samples using immunological procedures. Modulators of PDE8  
CC activity are useful in treating a wide range of diseases and  
CC physiological conditions in which PDE8 activity is known to be involved.  
CC The present sequence is human PDE8 A2 splice variant protein  
XX  
SQ Sequence 803 AA;  
Query Match 95.0%; Score 3997; DB 7; Length 803;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEDGSNNASCPRRUTECTLSPLTDEKAKAYLSLHPQVLDPEVSESVAETVEKMKRK 60  
DB 15 MEDGSNNASCPRRUTECTLSPLTDEKAKAYLSLHPQVLDPEVSESVAETVEKMKRK 74  
QY 61 TTKADESPKESVRYODTNMGGVYELNSYIEORLDTGGDNHLLLYELSSIIIRIATKAD 120  
DB 75 NTKSDEBAPKESVRYODTNMGGVYELNSYIEORLDTGGDNHLLLYELSSIIIRIATKAD 134  
QY 121 GFALYFLGECNNSLCVFIIPGMEQGPRLIPAGPITOGTTISAYVAKSRKTLVVEDILGD 180  
DB 135 GFALYFLGECNNSLCVFIIPGMEQGPRLIPAGPITOGTTISAYVAKSRKTLVVEDILGD 194  
QY 181 ERFPRGTGLESSTRIGSVCLPIYVAIGLILGLIELYRWMGEAFCLSHQEVATANTLAMA 240  
DB 195 ERFPRGTGLESSTRIGSVCLPIYVAIGLILGLIELYRWMGEAFCLSHQEVATANTLAMA 254  
QY 241 SVAIHQVQVCGRLAQOTBLNDPLDVSSTKYFDNIYVAIDSLLEHIMIYAKNLVNAIRCALF 300

Db 255 SVAIHQVQVCGRLAQOTBLNDPLDVSSTKYFDNIYVAIDSLLEHIMIYAKNLVNAIRCALF 314  
QY 301 QVDHKKKELYSDDLPIGEEKGKPIFKTKYKIRFSIEKGIAGQVARTGEVANIIPAYADP 360  
DB 315 QVDHKKKELYSDDLPIGEEKGKPVFKTKYKIRFSIEKGIAGQVARTGEVANIIPAYADP 374  
QY 361 RPNREVDLYTGTATNIIICMPPIVSRGSVIGVQVQNKISGSAFSTKDNNFMAVPCAL 420  
DB 375 RPNREVDLYTGTATNIIICMPPIVSRGSVIGVQVQNKISGSAFSTKDNNFMAVPCAL 434  
QY 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEMQGLMRFNLPARI CRDIELEHFDIG 480  
DB 435 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEMQGLMRFNLPARI CRDIELEHFDIG 494  
QY 481 PPNMMPGIFVYMIHRSCTGSCFELEKLCRTIMSYKRYRVPYNNMGAATVAHCAVTAI 540  
DB 495 PPNMMPGIFVYMIHRSCTGSCFELEKLCRTIMSYKRYRVPYNNMGAATVAHCAVTAI 554  
QY 541 LONNGLFTDLERKGLIACLDHKGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTV 600  
DB 555 LONNGLFTDLERKGLIACLDHKGFSNSYLQKFDHPLAALYSTSTMEQHHFSQTV 614  
QY 601 SIQLEGHNIESTLSSSEYEQVLEIRKAIATDIALYFGNRKQLEMYQTGSLNLHNS 660  
DB 615 SIQLEGHNIESTLSSSEYEQVLEIRKAIATDIALYFGNRKQLEMYQTGSLNLHNS 674  
QY 661 HRDRIYGLMTACDLCSTYKLMPTVKLTANDIYAFPAEGDEMKLGIOPIPMMDRDKRD 720  
DB 675 HRDRIYGLMTACDLCSTYKLMPTVKLTANDIYAFPAEGDEMKLGIOPIPMMDRDKRD 734  
QY 721 EYPOGQLGFYNAVAIPCTTTLTQILPTEPPLKACRDNLNOMEKVI RGEETAMWISGFP 780  
DB 735 EYPOGQLGFYNAVAIPCTTTLTQILPTEPPLKACRDNLNOMEKVI RGEETAMWISGFP 794  
QY 781 APSKSTPE 788  
DB 795 AQAASE 802

Search completed: January 10, 2006, 13:53:59  
Job time : 85 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:50:05 ; Search time 20 Seconds  
(without alignment)  
3829.427 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206  
Sequence: 1 MEDGSPNNASCRRRLTECLF.....GGPAPSKSTPEKLVAKVED 796

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	952	22.6	393	2 T25590	hypothetical prote
2	918	21.8	875	1 A48719	3',5'-cyclic-GMP p
3	912.5	21.7	875	1 JM0106	3',5'-cyclic-GMP p
4	909	21.6	921	1 A40981	3',5'-cyclic-nucle
5	897	21.3	928	1 UC2486	3',5'-cyclic-nucle
6	693.5	16.5	856	2 S30762	3',5'-cyclic-GMP p
7	693	16.5	858	2 JC4520	3',5'-cyclic-GMP p
8	689.5	16.4	854	2 A42828	3',5'-cyclic-GMP p
9	687.5	16.3	856	1 A47451	3',5'-cyclic-GMP p
10	684	16.3	853	2 A36617	3',5'-cyclic-GMP p
11	683	16.2	862	2 I50186	3',5'-cyclic-GMP p
12	679	16.0	859	2 A34810	3',5'-cyclic-GMP p
13	674.5	15.8	859	2 S13030	3',5'-cyclic-GMP p
14	666.5	15.8	859	1 S06418	3',5'-cyclic-GMP p
15	663.5	15.7	859	2 B34611	3',5'-cyclic-GMP p
16	660	15.8	800	2 S13032	3',5'-cyclic-GMP p
17	599.5	14.3	918	1 D88544	protein R08D7.6 [1
18	598.5	14.2	841	1 S24462	probable 3',5'-cyc
19	315.5	7.5	610	2 I67946	3',5'-cyclic-nucle
20	315.5	7.5	673	2 I61358	3',5'-cyclic-nucle
21	315.5	7.5	844	2 I53865	phosphodiesterase
22	315	7.5	539	2 T16769	hypothetical prote
23	314.5	7.5	536	2 I67945	3',5'-cyclic-nucle
24	312.5	7.4	859	2 AC2089	adenylate cyclase
25	312	7.4	859	2 S71626	3',5'-cyclic-nucle
26	307.5	7.3	584	2 B53109	3',5'-cyclic-nucle
27	307.5	7.3	672	2 I61259	3',5'-cyclic-nucle
28	307	7.3	886	2 A54442	3',5'-cyclic-nucle
29	302	7.2	562	2 I59143	cAMP phosphodiester

30	302	7.2	564	2 A40949	cyclic-AMP phospho
31	301	7.2	564	2 JC1519	3',5'-cyclic-nucle
32	301	7.2	736	2 I61354	phosphodiesterase
33	296	7.0	498	2 A47286	3',5'-cyclic-AMP p
34	292	6.9	777	2 S65543	3',5'-cyclic-nucle
35	290	6.9	450	2 UC7266	3',5'-cyclic-nucle
36	289	6.9	535	1 A46378	3',5'-cyclic-nucle
37	288.5	6.9	535	1 A44161	3',5'-cyclic-nucle
38	278	6.6	536	1 JC6129	3',5'-cyclic-nucle
39	277	6.6	267	2 B33904	cAMP phosphodiester
40	272.5	6.5	534	1 A44162	3',5'-cyclic-nucle
41	270.5	6.4	768	2 T10796	3',5'-cyclic-nucle
42	263	6.3	323	2 S55348	3',5'-cyclic-nucle
43	261.5	6.2	664	2 T24459	hypothetical prote
44	260.5	6.2	519	2 T14783	hypothetical prote
45	258.5	6.1	860	2 AB2044	adenylate cyclase

ALIGNMENTS

RESULT 1  
T25590  
hypothetical protein C32E12.2 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #next\_change 09-Jul-2004  
C/Accession: T25590  
R/Milcox, L.  
submitted to the EMBL Data Library, November 1996  
A/Description: The sequence of C. elegans cosmid C32E12.  
A/Reference number: Z20055  
A/Accession: T25590  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-393 <WIL>  
A/Cross-references: UNIPROT:P91119; UNIPARC:UPI000013A3FB; EMBL:U80032; PIDN:AB53879.1;  
A/Experimental source: strain Bristol N2; clone C32E12  
C/Genetics:  
A/Map position: 1  
A/Intons: 52/2; 137/2; 166/2; 217/3; 327/2  
F:189-393/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 22.6%; Score 952; DB 2; Length 393;

Best Local Similarity 48.4%; Pred. No. 2.2e-63; Matches 191; Conservative 69; Mismatches 127; Indels 8; Gaps 5;

QY	336	IEKGIAGVARTGEVNTIPDAVADPRFNRVDLYGTTNTILCMPIVRSVIGVQWV	395
DB	1	MSKGIAGVASTGEGINENVAEDERFNDVDSKTYTTKILCMPILRGIYGVQWV	60
QY	396	NKISGSAFSEKTDENNEKMFVFCALALHCAANNYHRIHSECIYRTMELSYHSICTSEB	455
DB	61	NKHDG-VFTRQDEDAEIRAVYCGALHHAUKYDKIRSEQKRVALLVLAHVSVCNAD	119
QY	456	WQGLMFNLPARICRDIIEFHED--IGPENNWPGI FYTMHNR-SCGSGFELKLCRF	511
DB	120	VNKLKKEIENNRIV-ELETIDFGMKLSLEK--PLVAYVMEKTLRADTLRFPTEDLIRF	176
QY	512	IMSVKKNYRRVPYHNMKAVTAHCVYALIONNNGFTLERKGLLIACIChDLDRGFS	571
DB	177	VLTVRKNYRRVAVAHNAHGSVAHNAFATLMSPDNFTLEALALVSCICHLDRGKN	236
QY	572	NSYLQKFDHPLAALVSTSTWQHFPQTVSIQLGHNITFSTLSSEYEQVLEIRKAI	631
DB	237	NAYMKTMSTPIASIVSTVSWERHFNQVTYTIQQDGNILKSLSSDYKKTLSLKHCL	296
QY	632	ATDLALYFGNRKQLEMYTQGSIMLNQSHRDRVIGLMMTACILCSVTYKLMPTKLTAND	631
DB	297	ATDLALFFSKAKATLANTVNTFTDIRROEHRLLTQAVMTGCLVASAKPMNIQTETVKV	356
QY	692	IYAEFWAGDEMKGLGIQPIPMMDRKRDEVPQCG	726

Db 357 IFBEPYDQDABRUSGKEPIPMWDRQQAHLMPQW 391

RESULT 2

A48719 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine

N:Alternate names: PDB5A1

C:Species: Bos primigenius taurus (cattle)

C>Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 26-Aug-1999

C:Accession: A48719, A35807

R:McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecsek, A.; Seger, D.; Le Trong, H.; Colbr

J. Biol. Chem. 268, 22863-22873, 1993

A:Title: The structure of a bovine lung cGMP-binding, cGMP-specific phosphodiesterase de

A:Reference number: A48719, MUID:94043054, PMID:8226796

A:Accession: A48719

A:Molecule type: mRNA

A:Residues: 1-875 <MCA>

A:Cross-references: UNIPARC:UPI000014645D, GB:L16545

A:Experimental source: lung

R:Thomas, M.K.; Francis, S.H.; Corbin, J.D.

J. Biol. Chem. 265, 14971-14978, 1990

A:Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding

A:Reference number: A35807, MUID:90368672, PMID:2168396

A:Accession: A35807

A:Molecule type: protein

A:Residues: 90-101 <THO>

A:Cross-references: UNIPARC:UPI000017289B

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A, 3',5'-cyclic-nucleotide phosphodie

C:Keywords: alternative splicing, cGMP binding, phosphoprotein, phosphoric diester hydro

F:602-825/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

F:92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict

Query Match 21.8%; Score 918; DB 1; Length 875;

Best Local Similarity 30.2%; Pred. No. 2.6e-60;

Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

10 SCFRRLTSCPLSPSLTDE-----KYKAY---LSLHPVLTDE-----FVSEVSAR 51

68 SC-----SCPLQPSRAESSVGTTPRKISASBPRLPIYKISGVSLSDDKKE 122

52 TVEKWLKRTNKADESPKEVSRVQDTNMGVVELNSYIEQRLLDTGDNHLLYEISS 111

123 QMPLTSPRFNDDEGQCSR-----LLELVYDISHLDVVALCHKIFLHNG 168

112 IIRIATKADGFLYLVGECNNSLCVFIIPGMEGQRLIPAGPIQGTT----- 160

169 LI-----SADRYSLFLVCESSNDKFLI-----SRLEF---DVAEGSTLEEVANNICRL 213

161 -----ISAVNAKSRKTLVEDILGDERFPRGTGLESSTRIGSVLCPIYTAIGDILGILE 215

214 EWNKGIQGVHVAFFGEPLNIKDAYEDPRFAEVDQITGYKTQSILCMPIKNHEEVAVQAQ 273

216 LY--RHMGKEAFCLSHOEVAATNLMASVAIHQOVQCRGLAKQTEINDFLDVSKTYPDN 273

274 AINKSGNGGFTBDEKOPFAVLAFCGIVLHNAQYETSLLENKRNQVLDLASLIFRE 333

274 IVAISLSLEHMITVAKNLVNAIDRCALFOVDHAKKELYSPLPDIGEKKEGKPIFKTKKEIR 333

334 QOSLEVIILKKIAATLISFQVQKCTIFIVDEDCSDSFSSVFMECEBELEKSSDTLTREND 393

334 PS-IEKGIAQGVARIGEVLNIPDAVADPRF---NREVDLYGTGTTRNILCMPIVS--RGS 387

394 ARIRIYMTAQYKNTMEPLNIPDVSKDKFPPWTNENNGINQOCIRSLCTIYIKGKKAK 453

388 VIQVQVQVNTKISGS-----AFSKTDENNFKMAVFAFCALALHCAANYHRIHSECIYRVTM 442

454 VIQGVQVQVNTKISGS-----AFSKTDENNFKMAVFAFCALALHCAANYHRIHSECIYRVTM 442

454 VIQGVQVQVNTKISGS-----AFSKTDENNFKMAVFAFCALALHCAANYHRIHSECIYRVTM 442

443 EKLSYHSICITSEEWQGLKRFNLPARI-----CRDIELFHPDIGPFENMPPGIFVTMI 494

514 EYLSYHASAAEETRELQ---SLAAVVPASAQTLKITDPSFSDLEFSLDETALCTIRMFED 571

495 HRSCTSCPELEKLCRFIMSVKQYRR-VPIYNNKGAIVAVAHQAYALLQNN--NGLFTDL 551

Db 572 LNLVONFQMKHEVLCKWILTSVKKAYRKVAVYNNRHAFNTAQOCWFALKAKGIQKRLTDL 631

552 ERKGLITLCLCHDDHREFSNSYLQKPDHPLAALYSTMEQHHFSQVSLTQLEGHNIF 611

632 EIALLLALSHDLDHRRGVNNSYIQSRSHPLAQLYCHSIMHHHHDDCLMLNSFGNOL 691

612 STLSSEYEOVLLEIRKAIITADLALYGNRKQLEMYQTSGLMLHNSHRRDVLGMNT 671

632 SGLSIEBEKTKTLIKIKAILTDALYIKRGEFFELIMKQFNLEDHOKELFLAMLMT 751

672 ACDCSVTKMPVTKLTANDIYAEFMAEGD-EMKGLGIQIPMDRDRDREVPQQLGFR 730

752 ACDSLAIKTPMPIDQRIAEVLATEFFDQDRREKELNIEPADLNNREKKNKIPSMQVGF 811

731 NAVAIPCTTITQLIPREPIILKACRDNLNMEKVIKREERFAMTSG 777

812 DAICQLVETLTHVEDCFPLDGCRRKRRQKQALAEQOKETL-ING 857

RESULT 3

JW0106 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human

N:Alternate names: PDB5A1

C:Species: Homo sapiens (man)

C>Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 09-Jul-2004

C:Accession: JW0106

R:Stacey, P.; Rulien, S.; Dapling, A.; Phillips, S.C.

Biochem. Biophys. Res. Commun. 247, 249-254, 1998

A:Title: Molecular cloning and expression of human cGMP-binding cGMP-specific phosphodie

A:Reference number: JW0106, MUID:98308101, PMID:9642111

A:Accession: JW0106

A:Molecule type: mRNA

A:Residues: 1-875 <STRA>

A:Cross-references: UNIPROT:O76074, UNIPARC:UPI000003406D, GB:AJ004865, NID:G3355605, PIT

C:Gene: GDB:PDB5A

A:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A, 3',5'-cyclic-nucleotide phosphodie

C:Keywords: alternative splicing, cGMP binding, phosphoprotein, phosphoric diester hydro

F:612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

F:102/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict

Query Match 21.7%; Score 912.5; DB 1; Length 875;

Best Local Similarity 31.2%; Pred. No. 6.8e-60;

Matches 238; Conservative 136; Mismatches 321; Indels 69; Gaps 18;

61 TNKANDBSPKESVRY--QDTNMGVVELNSYIEQRLLDTGDNHLLYEISSIIRIATK 118

126 SDSEKKEGMPITPRPFHDEGQCSRLELVYDISHLDVVALCHKIFLHNGLI-----S 181

119 ADGFALYLVGECNNSLCVFIIPGMEGQRLIPAGPIQGTT-----IS 162

182 ADRYSLFLVCESSNDKFLI-----SRLEF---DVAEGSTLEEVANNICRLNNKGI 230

163 AVNAKSRKTLVEDILGDERFPRGTGLESSTRIGSVLCPIYTAIGDILGILEY--BHW 220

221 CHVALGEPPLNIKDAYEDPRFAEVDQITGYKTQSILCMPIKNHEEVAVQAALINKSG 290

221 GKEAFCLSHOEVAATNLMASVAIHQOVQCRGLAKQTEINDFLDVSKTYPDNVAIDSL 280

221 NGGFTBDEKOPFAVLAFCGIVLHNAQYETSLLENKRNQVLDLASLIFREQOSLEVI 350

291 LEHMITVAKNLVNAIDRCALFOVDHAKKELYSPLPDIGEKKEGKPIFKTKKEIRFS-IEKG 339

351 LKKIAATLISFQVQKCTIFIVDEDCSDSFSSVFMECEBELEKSSDTLTRENDAKINYM 410

340 IAGQVARTGEVLNIPDAVADRENREVDLYGYTT---RNILCMPIVS--RGSYIGVQ 393

411 YAOYKNTMEPLNIPDVSKDKFPPVTE--NTGANNVQOCIRSLCTIYIKGKKAKYIGCQ 469

394 VNKISGSA-----FSKTDENNFKMAVFAFCALALHCAANYHRIHSECIYRVTMKLSYH 448



Db 470 LVNKEBNTGKPKPRNDEQLEAVIFCGIGIONTOYWEAVERAMAKONTLELVSH 529  
Qy 449 SICTSBEMOGLMRPNLPARI-----CRDIELFHFDIGFENNMPGIFVYMIRHSCGT 500  
Db 530 ASABEETRELQ--SLAAVVPVSAQTLKITDPSFSDIELSDLETALCTIRMTDLNLVON 587  
Qy 501 SCPELEKLCRFIMSVYKKNRR--VPHNMKGAVTVACWAIL-----QNNGLFTDLERK 554  
Db 588 PQMKIEVLCRWILSVKKNRKNVAVYNNHRAFTACQMPALAKGKIQNK---LTDLETL 644  
Qy 555 GLLIICLCCHDLDRGFSNSYLQKFDHPPLAALYSTSTMEQHFSSQVYSIQLBGNIFSTL 614  
Db 645 ALLIALASDLDRKGVNNYSIQSEHPPLQLYCHSIMEHHNFDQCLMILNSFGNQLSG 704  
Qy 615 SSSBYEQVLEIRKAIATDLALYFGNRKQLEBMYQVGSILNHOSHNDRVIGLMTACD 674  
Db 705 SIEBKTKTKIKQKAILATDLALYIKRGDFEFLIKRQNFLEDPHQKELFLAMLTACD 764  
Qy 675 LCSVTKLAVTVLTANDIYAEFMAEGD-EMKGLGIQPIPMDBDKRDEVPOQLGFYNAV 733  
Db 765 LSAITKPMPIQORIALVELVATEFPDQDRRKELNIEPTDLNREKKNKIPSMQVGFDAI 824  
Qy 734 ALPCTTLTQILPPTBPLKACRDNLQMKVIRGSETAMWISG 777  
Db 825 CLQYEAALTHVEDCFPLDGCRRKQKQALLAEQOE-KMLING 867

RESULT 4

A40981  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine  
N:Alternate names: cGMP-dependent phosphodiesterase  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 26-Aug-1999 #sequence revision 26-Aug-1999 #text change 09-Jul-2004  
C:Accession: A40981; B36112; A36112; B26650; A60179; C26650  
R:Sommerburg, W.K.; Mullaney, P.J.; Beavo, J.A.  
J: Biol. Chem. 266, 17655-17661, 1991  
A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase  
A:Reference number: A40981; MUID:91373395; PMID:1654333  
A:Accession: A40981  
A:Molecule type: mRNA  
A:Residues: 1-921 <SON->  
A:Cross-references: UNIPROT:P14099; UNIPARC:UPI0000127BB; GB:M73512; NID:g162829; PION:  
R:Le Trong, H.; Beier, N.; Sommerburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Cha  
Biochemistry 29, 10280-10288, 1990  
A:Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiesterase  
A:Reference number: A36112; MUID:91104948; PMID:2176866  
A:Accession: B36112  
A:Status: not compared with conceptual translation  
A:Residues: 592-921 <LEFT>  
A:Molecule type: mRNA  
A:Cross-references: UNIPARC:UPI0000172895  
A:Accession: A36112  
A:Molecule type: protein  
A:Residues: 1-203, 'D', 634-794, 808-868 <CHTA>  
A:Cross-references: UNIPARC:UPI0000172895  
A:Residues: 613-632, 'L', 634-794, 808-868 <CHTA>  
A:Cross-references: UNIPARC:UPI0000172897; UNIPARC:UPI0000172898  
A:Experimental source: heart  
R:Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacel, E.; Murashima, S.; Manganuel  
Second Messengers Phosphoproteins 13, 87-98, 1991  
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-st  
A:Reference number: A60179; MUID:92065414; PMID:1659635  
A:Accession: A60179  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 311-803, 'DV', 806-921 <TAN>  
A:Cross-references: UNIPARC:UPI0000172899

A>Note: part of this sequence was confirmed by protein sequencing  
C:Comment: This protein is not glycosylated.  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-  
C:Keywords: acetylated amino end; alternative splicing; cAMP binding; cGMP binding; homoc  
F:635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 21.6%; Score 909; DB 1; Length 921;  
Best Local Similarity 31.1%; Pred. No. 1.3e-59;  
Matches 254; Conservative 142; Mismatches 306; Indels 114; Gaps 27;

Qy 16 TEEPLSPSLTDE--KYKAVLSIHPQLDFEVSVAETVEK-----LKRKNKADPS 69  
Db 122 TQVAVIPLVDKAGAAVAVILVHCGQLSD--NEEMSLQAVEGHTLVALKRVOALQORESS 179  
Qy 70 -----PKESVRYODTNMGVVYELNSYIEQRLDTGSDNHL-----LYELSS---- 111  
Db 180 VAPKATQNPPEBAADQ-----KGVAV-----TNQDRKILQCGELYDLDASSIQ 225  
Qy 112 -----IIRATKADGRLALYFLGECNNSL--CVPIPKMGKGGPRLIPAGPIQGTTISAVY 165  
Db 226 LKVLQYLQOEQASRCCLLVSEDMQLQSKVIGDKVLEESISF-----PLTGRLL--GGV 279  
Qy 166 AKSRKTLVEDIIGDERFPGTGLS--GTRIQSVLCPIYV--AIGDLIGILELYRMWK 222  
Db 280 VEDKKSIAQKDLTSRDM-----QQLQSMGCEVQAMLCVPVIRATVDQVVALACAFKLG 335  
Qy 223 EAFCLSHOEVAATAMASVAIHQVOCRLAKQTELN-----DPLVDYSKYFPDNIYAI 277  
Db 336 DLFTQDEHVIQCHFYSTVLTST-----LAFQEQKLCCECOALLVQAKVLFHTLDV 390  
Qy 278 DLSLHIMTYAKVYNADRCALFOVDHKKELXSLDFDGEKEKPIFKTKKEIRFSIE 337  
Db 391 SVTLDEITTEANLSNAELCSVFLD--QNELVAVFPD-----GQVDESEYIRHPAD 442  
Qy 338 KGIAGOVATGEVNLINPDAYADPRFNEVDLYGTTRNIIICMPTYSRS--SVYGVQVYN 396  
Db 443 QGIAGVATTTQGLINIPDAIYHPYRGVDBDGTGRTNIIICPIKNEQEVIGVAVELN 502  
Qy 397 KISGAFSKTDENNPFMAVFCALALHCANMYHRIHSECIYVTEKLSYHSICTSEB 456  
Db 503 KINGPWFSKFEDDLATVAFSIGIASHSLYKVAEQYRSHLANEMMYHMKVSDDEY 562  
Qy 457 QGLMRPNLPARICRDIELHFPIGP-----FENMMPGIFVYMIRHSCGS 501  
Db 563 TYKLDHGIQPVAAIISNFASFYTPRSRPEDDTSMALSLQDM--NFINNKKIDCPT- 618  
Qy 502 CPELEKLCRFIMSVYKKNRVRPYHNMKGAVTVACWAILQON--NNGLFTDLERKGLIA 559  
Db 619 -----LAPFCILNVKKGIDPPIYHNMHAFVSHPFCILYKQLELTNYLEDNEIFALFIS 672  
Qy 560 CLCHDLDRGFSNSYLQKFDHPPLAALYST--STMEQHFSSQVYSIQLBGNIFSTLSS 617  
Db 673 CMCHDLDRHGTNNSPGVASKSVLAALYSEBGSMEHHRPAQALAIINTGNCIFFDHSRK 732  
Qy 618 EYBQVLEIRKAIATDLALYFGNRKQLEBMYQVGSILNHOSHNDRVIGLMTADLCS 677  
Db 733 DYQRMIDLKRDIIATDLALNHILRFIDLOKMAEVG--YDRTNQSHSLCLCLMTSCDLS 791  
Qy 678 VKTKLAVTVLTANDIYAEFMAEGDKKLGIOPIPMDBDKRDEVPOQLGFYNAVAPC 737  
Db 792 QTKGMKTKTKIKABLYKEFSQGDLEKANKGNRPMKMDKEKA-YIFELQISFHEHLMPI 850  
Qy 738 YTTLTQILPPTBPLKACRDNLQMKV-----IRG 768  
Db 851 YKLLQDLFPKALVELYRVASNREHWTKVSHKFTIRG 886

RESULT 5

JC2486  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat  
N:Alternate names: cGMP-dependent phosphodiesterase  
C:Species: Rattus norvegicus (Norway rat)

CDate: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 09-Jul-2004

CAccession: UC2486

RiYang, Q.; Baskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein

Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994

A>Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.

A|Reference number: UC2486; MUID:95110334; PMID:7811274

A|Accession: UC2486

A|Molecule type: mRNA

A|Residues: 1-928 <YAN>

A|Cross-references: UNIPROT:Q01062; UNIPARC:UP10000127BEC; GB:U21101; NID:9706929; PIDN:

A|Experimental source: brain

A|Experimental family: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-

C|Keywords: alternative splicing; cAMP binding; cGMP binding; homodimer; phosphoprotein;

F|643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NPDP>

F|619/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 21.3%; Score 897; DB 1; Length 928;

Best Local Similarity 30.2%; Pred. No. 1,1e-58;

Matches 248; Conservative 152; Mismatches 292; Indels 130; Gaps 27;

16 TECTLSPSLTDE--KVKAYLISLPQVDEPFVSEVSVAETVKW---LKR-----59

134 TQVAVIPFLDKETGTVAIVLVHCGQLSD--SEEQSLQVVEKALVALQVVALQGRPR 191

60 -----KTKKADDESPKREVSRYQDTNMQ--GVWYEIENS-----YIERDLTGSDNH 103

192 AVQNTSAPDSQDQDEKGYATADRKLQLCGELYDLDTSLQLKVLRLQ--ETQATHC 249

104 LLLVELSIIIRIATKADFALYFLGECNNSLCVFIIPQMKEGORPLIPAGPIYTGTTISA 163

250 CLLVSEBNLQDSKVIGEKV--LGE-----EVSFPLTMGRLL--G 285

164 VYAKSRKTLVLEDILGDERPFRGTGSEGTRIQSVLCLPIVT-AIGDLIGILELYRMHGK 222

286 QVVEDKQCIQKDLITSDVDQQLQNMWL--GCELRAMLGVPISRATDQVVALACAFNKLGG 343

223 EAF-----CLSHQ--EYATANLMAASVAIHQVQVCRGLAQTELPDLVDVSTYF 271

344 DFFDEDEDERAIOHCCHYGYTGLTSTLAFQK--BQKKCECOA-----LIQVAKNLF 392

272 DNIYALDLEHIMIVAKNLVNAIDRCALFOVDHKKKELYSDFPIGEEKGKPIFFKTKTE 331

393 THLDVSVLLDEBITREARNLSNAELCSYFLD--QNELVAVCFD-----GGVVDDESYE 444

332 IRFSIEKGIAGQVARTGEVLNIPDAVADPRFRREVLYTGTTNNILCMPIVSRG--SVIG 390

445 IRIPADQGIAGHAVTTGQILINIPDAVAHPLFYRGVDSGTGRTNNILCFPIKHNQGVIG 504

391 VVQWVNTKISGSAFSEKTDENNFRMAVFCALALHCANNYTHIRHSECIYRYTMELSTHST 450

505 VAEIVNNKINGPWFSEKFEEDLATAFSICYGISIAHSLYKKNBAQYRSHLANNEMMYTHMK 564

451 CTSEBMOGLMRFNIPARICRDIELFHPDIG-----PENMMPGIFVYMIH 495

565 VSDDEYTKLHDGQIOPVAIDSNFANFTYTRSRSLPEDDTSAIISLMQDM---NFINNYK 621

496 RSCGTSCPELEKLCRFIMSVKXNRYRVRPYNMKIAVTVAHCMYAILQN--NNGFLTDLER 553

622 IDCPY-----LARFCIMVKKGYRDPYHNMMAFVSHPCYLLYKNGLEISNLYDEI 674

554 KGLLIACIChULDHRGFSNSYLQKFDHPLALYST--STMEQHHSQCTVSLQLEGNHIF 611

675 FALFISICCHLDLHRGTNNSPFVASKVTLALYSSEGSVERHHFPAQALALNTHGNCIF 734

612 STLSSEVEOULEIRKAIITATDLALYFGNKKOLEBMYQGSLLMHNQSHDRYIGLMT 671

735 DHFSKQDQRMQLDRDIIILATDLNHHIRIKFDLQKALEVG--YRRNNQHHRLILCLMT 793

672 ACDCISVYKLVKPYKTLTANDIYAFFWAGDEMKLGIQIPIWMDRDXRDEVQCOLGFYN 731

794 SCDLSDQKMGKTKRIKLAELLYKFFSGDGLDKAMGNRPMEMDRERKA--YIPELQISFME 852

732 AVAIPCYTTTLQILPTEPBLIKACRDINLQWKEV----IRG 768

Db 853 H1AMP1YTLQDLFPKRAALYERVA5NRHETWKVSHKFTIRG 894

RESULT 6

S30762

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse

C|Species: Mus musculus (house mouse)

C|Date: 22-Nov-1993 #sequence revision 19-Oct-1995 #text\_change 09-Jul-2004

C|Accession: S30762; S13031; S13121

R|Baehr, W.

submitted to the EMBL Data Library, June 1991

A|Reference number: S30762

A|Accession: S30762

A|Status: preliminary

A|Molecule type: mRNA

A|Residues: 1-856 <BA05>

A|Cross-references: UNIPROT:P23440; UNIPARC:UPI00000405A; EMBL:X60133; NID:G53595; PIDN:R|Baehr, W.; Champagnon, M.S.; Lee, A.K.; Plettl, S.J.

FEBS Lett. 278, 107-114, 1991

A|Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha-chain of the beta-subunit gene.

A|Reference number: S13030; MUID:91130581; PMID:1847109

A|Accession: S13031

A|Status: preliminary

A|Molecule type: mRNA

A|Residues: 1-559, 'G', 561-856 <BA2>

A|Cross-references: UNIPARC:UPI00001759BC; EMBL:X60133

R|Bowers, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.

Nature 347, 677-680, 1990

A|Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subunit cGMP phosphodiesterase gene.

A|Reference number: S13121; MUID:91015387; PMID:1977087

A|Accession: S13121

A|Molecule type: mRNA

A|Residues: 1-2, 'X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-235, 'A'.

A|Cross-references: UNIPARC:UPI0000161CP2; EMBL:X5968; NID:G53616; PIDN:CAA39439.1; PID: C|Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide pC|Keywords: cGMP binding; phosphoric diester hydrolase

F|556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.5%; Score 693.5; DB 2; Length 856;

Best Local Similarity 25.3%; Pred. No. 1.7e-43;

Matches 226; Conservative 165; Mismatches 332; Indels 169; Gaps 31;

23 SLTDEKVAAYLTHPOVLDEPVSESVSAETV-----EKWLK-----RKTNKAKDESPK 72

2 SLSEQVAVSPFDGNTPAHQYFGKTLSPENVAGACDGLADGSLRELCOVESALFE 61

73 V-SRYQDTNMGVVYELNYSYFORLDT---GQDNHLLY-ELSSITRIATKADGFLLY- 125

62 LVQDQESVNMNERVVFK-----ILRLCTILHADRCSLFMYRQNGIAELATRL--FSVQ 115

126 --FLGECNNLSCLVFLPQMKEGQPRLLIPAGITGCTTISAYAVKSKTLLVEDILGDERF 183

116 DSLIEDC-----LVPPDSE-----IVPLDIG--IYGHVAQTKMIVQVAESCPHF 160

184 PRGTGLESSTRIQSVLCPIYTAIGDLIGILELYRHMGEAFCLSHOEVAATAMAVASV- 242

161 SSFADDELVDYTKNLISPIWNG-KDVAVIVAAVNNLDGCPFSBEDVDVTKLYNFATLN 219

243 -----AIHQVQCRGLAKQOTELNDFLIDVSKTYFDNIVALIDSLHEIMTYAKNLVNAD 295

220 LKIYHLSTYLNCESTRG-----QVLLMSANKVFEBELTIERQFHKAFTYRAYLNCE 271

296 RCALPQVDHKKKELYSDFDI--GEK-----EGKFI--FKKT-----KEIR--- 333

272 RYSVGLDLMTEKEKFFDVPVPLVMGEAPYSGRPTGRGRIVFYKVIDYILHGKEDIKVI 331

334 -----FSIEKGIAGQAVATGEVLNI PDAYADPRFV-REVDL- YTGYYTNILCMPIVS- 384

332 TRPADHMLAAGLPTTYVAESGFTICINMNASADBMRFQCGPDLDDSGWIKVKNVLSMPIVNK 391



A>Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBI:109784)  
 R.Khranov, N.V.; Feshchenko, E.A.; Snelova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki  
 PBBS Lett. 327, 275-278, 1993  
 A>Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu  
 A:Reference number: S34590; MUID:93351644; PMID:8394243  
 A:Accession: S34590  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-854 <NR>  
 A:Cross-references: UNIPARC:UPI000012731; EMBL:X66142; NID:g336492; PION:CAA6932.1; PI  
 R:Weber, B.; Reese, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowdel, D.; Andrew, S.; Sc  
 Nucleic Acids Res. 19, 6263-6268, 1991  
 A>Title: Genomic organization and complete sequence of the human gene encoding the beta-  
 A:Reference number: S18715; MUID:92066478; PMID:1720239  
 A:Accession: S18715  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-314, 'Q', 316-319, 'L', 321-359, 'R', 361-697, 'I', 699-854 <WEB>  
 A:Cross-references: UNIPARC:UPI000016A6BE; EMBL:X62694  
 A:Genetics:  
 A:Gene: GDB:PDEB, PDEB  
 A:Cross-references: GDB:125915; OMIM:180072  
 A:Map position: 4p16.3-4p16.3  
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P  
 C:Keywords: cGMP binding; phosphoric diester hydrolase  
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
 Query Match 16.4%; Score 689.5; DB 2; Length 854;  
 Best Local Similarity 24.7%; Pred. No. 3,3e-43;  
 Matches 219; Conservative 165; Mismatches 343; Indels 159; Gaps 28;  
 23 SLTDEKVAVSLHPOVDFEVSASAEVY-----EKMILKRTNKAKD-----EPSPKEVS 74  
 2 SLSEQASPLQNDPFAQYFKKSLSPNVGRGCGDCCPPCDSLRDCQVEESTALIE 61  
 75 RYQD-----TNMQGVYELNSYIEORLDTGDNHLLLYELSSITRIATKADGFLY---FL 127  
 62 LVQDQGESIMRERVYFKVIRLCITLLQADRCSLFMYRQNGVAELATRL--FSVQPDSTL 119  
 128 GECNNSLCVFPPEKKEGQRLIPAGPTIGTTISAVYAKSKRTLLVEDILDERPPRGT 187  
 120 EDC-----LVPPDE-----IVFPLDIG--VVGHVQTKKMNVEDVACPHSSPA 164  
 188 GLESGTRIQSVCLPIVTAIGDLIGILEYRHMGEAFCLSHQEVATNLAAVY----- 242  
 165 DELTYKTKNMLATPTIMNG-KQVAVYMAVKNLGNPFPSBEDVFLKTLNFAITLTKY 223  
 243 ---AIHQVQVCGGLAKQTELANDPLDVSKTYEPDNIYALISLEHIMITYAKNLVNDRCAL 299  
 224 HLYSLHNCETRG-----QVLLMSANKVFEBELDIERQHKAFYTVRAVLANCERYSV 275  
 300 FOVDHKNKELYSDDLFDI--GEKK-----EGKPI-FKKT-----KEIR----- 333  
 276 GLLDWTKEKEFPDQSVLMGESQPYSGPRTPDGRIBLVFYKVIDYILHGKEIKVLPESA 335  
 334 --FSLEKGIAGVATGEVLNTPDAVADBRFRNREVDLY--TGYYTNILCMPTIVS-RGSV 388  
 336 DHWALASGIPSYVASGFTCNTMNASADMEFKQEGALDSDGMLIKNVSIMPIVANKKEI 395  
 389 IGVQVQVVKISSASKTDENNFKMFAYECALALICANNYHRIHSECIYRTMEKLSYH 448  
 386 VGVAFYVRKQKQKPPDEQDEVLMESITOPFLGKSVANTDITYDKANLENKODIADQMVLYH 455  
 449 SICTSEEMQ-----GIMRPNLPARICRDIELHFH--DIGPE 483  
 456 VACDDEIDQLIPTRARLKEPADCEDEDELGELIKKEELPPTFDIYEBHFDLCTEILD 515  
 484 NMMPPIFYVMIRSCGTSFEL-----EKLCRFIMSKVQKVRPRPYNMHGAATV 533  
 516 LVKCIQWY-----YELGVVRKFOIPEVAVRFLPFSISKGRIRITYNMHRGENV 565  
 534 AHCMVAIIQNN--NGLFTDLERKGLLIACLDLHGRFSNSYLQKFDPLAALYSTSTM 591

DB 566 AQWTFLLMTGKLKSYTDLNFAVNTAGLCHDIDHRGTNNLYOMKQNPFLAKHGSSIL 625  
 QY 592 EOHHSQSVTSLIQEGHNIPTLSSESEYOYLEIRKAIITDIALYGNRKQLEEM--- 648  
 DB 626 EKHHLPEKFLISESTLNIYONLNRQSHVYHMDIILITDILYIKKRAMPOKIYDE 685  
 QY 649 ---YQTGS-----LNIHQSHRDRIYGLMNTACDLCVYTKLMPYTKLTANDIYAEFMAEG 700  
 DB 666 SKNYDDKSWVEYLSLET--TRKEIYMAVMMNTACDLSAITKEPVEVQSKVALLVAFEFMEG 744  
 QY 701 D-EMKGLGIOTIPMMMDRDKRDEVPQGGQGFNAVAIPCTYITLTQLPTEPEPLKCRDL 759  
 DB 745 DLERTVLQOQPIPMMDRNRKAEPLQVGFDFVCTFYKEPSRPHBEITLPFRLQNNR 804  
 QY 760 NOW-----EKVIRGETAMWISGPPAPSKST 786  
 DB 805 KEMKALADEYKAKVAKLEKEEBEERVAANKVGTICNGPAPKST 850  
 RESULT 9  
 A47451  
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: A47451; S34290  
 R:Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993  
 A>Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation i  
 A:Reference number: A47451; MUID:93248211; PMID:8387203  
 A:Accession: A47451  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-856 <SUB>  
 A:Cross-references: UNIPROT:P33726; UNIPARC:UPI00001728BD; GB:Z23014; NID:g312327  
 A:Experimental source: Irish setter, retina  
 A>Note: sequence inconsistent with the nucleotide translation  
 R:Clements, P.J.  
 submitted to the EMBL Data Library, June 1993  
 A:Reference number: S34290  
 A:Accession: S34290  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-184, 'D', 186-856 <CIB>  
 A:Cross-references: UNIPARC:UPI000012730; EMBL:Z23014; NID:g312327; PION:CAA80557.1; PI  
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p  
 C:Keywords: cGMP binding; phosphoric diester hydrolase  
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
 Query Match 16.3%; Score 687.5; DB 1; Length 856;  
 Best Local Similarity 25.2%; Pred. No. 4,7e-43;  
 Matches 225; Conservative 151; Mismatches 346; Indels 171; Gaps 26;  
 23 SLTDEKVAVSLHPOVDFEVSASAEVYKMKLRTNKAKDPSPEVSRVYD---T 79  
 2 SLSEQVQHPLQNDPFDQYFGKTLSPENVA-----GACGSGQPTDCASFRELQY 53  
 80 NMQGVYELNSYIEORLDTGDNHLLLYELSSITRIATKADGFLYFLGECNNSLCVFP 139  
 DB 54 BESALPFLVQDMQSVMMRERVFKILRLCTILR---ADRCSLFMYRQR----- 101  
 140 PQMKEGQRLIPAGITQTTIS-----AYYAKSKRTLLVEDILGD 180  
 DB 102 -GVAEIATRLFSVP--GSAIEDCLVPPDSEIYFPLDIGVGHVAAQTKKMNVDVIEC 157  
 QY 181 ERFPRGTGLESGTRIQSVCLPIVTAIGDLIGILEYRHMG-----KEAFCLSHQEVAT 234  
 DB 158 PHFSPFADELGYERNILATPTIMNGKEVAVYMAVKNLTDGCFPSBEDVFLKTLNFGT 217  
 QY 225 ANLAAVYA-IHQVQVCGGLAKQTELANDPLDVSKTYEPDNIYALISLEHIMITYAKNLVN 293  
 DB 218 LNLKLYHLSYLNHNCETRG-----QVLLMSANKVFEBELDIERQHKAFYTVRAVLYN 269

QY 294 ADRCALFQVDHKNKELYDLDLFDI-----GEE-----KEGKPI 325  
 DB 270 CDRYSVGLDMDTKKEKFEFDVMPVLNGEAQPSGPRTPDREIVFYKVIDYILHGKEDIKV 329  
 QY 326 FKTKTEIRPSIEKGIAGQVARTGEVLNIPDAVADPRFN-REVDL- YGYTTRNIIICMPYV 383  
 DB 330 IPSPADHMAIASGLPTTVASGFIICNMTNAADEMTFTQGEPLDSDGVINQVLSMPTV 389  
 QY 384 S-RGSVIGVQVQWVKISGSASFSTDENNKMPAVFCALALHCANNYHRIHSECIYRVTM 442  
 DB 390 NKKKEIIVGATFYNNKDKGKPFDEQEVLMESLTQFLGMSVLTMTDFYDKNKKLENKIDIAQ 449  
 QY 443 EKLSTHSITSTSEWQGLM---RPNLPARICDIDILFPHDIDGPFENMWG---IFVYMH 495  
 DB 450 DMVLVHVRCDDKDEIQILPTFRERLKEKPADCEDELGIL-----LKEVLPGPSKFDIYEFH 505  
 QY 496 RS-----CGTSC-FEL-----EKLCPFMSYKQYRVRYNNMKAAVTV 533  
 DB 506 FSDLECTELKLVKCGIQMYTELGAVRKFOIPQEVLRVLFPSYSKGYRRIITYNNMRGFRV 565  
 QY 534 AHCMYAILQNN--NGLFTDLERKGLLIACLDHLDHGFNSNYLQKFDHPLAALYSTSTM 591  
 DB 566 AQTMTPLTLTGKLSKSYTDLDEAFAMVTAGLCCHDIDHRTNNLYQMSQNPPLAKHGSSIL 625  
 QY 592 EOHHSQTVSIIQLGHNIFSTLSSEYQVLEIRKAIITADLALYFGNRKOLEMYOT 651  
 DB 626 EHHHLEFGKFLSEETLNIYQNLNRQHSHVHIMDAIITADLALYFKKRTMFOKIVD- 684  
 QY 652 GSLINLHNSHRDR-----VIGLMTACDLCSVTKLMPVTKLTANDIYAE 695  
 DB 685 -----ESKNYEDRKSNWEYLSLETRKEIIVMMAMMTACDLSATKMEVQSKVALLVALE 739  
 QY 696 FNAEGD-EKKKGIGIOPIPMDRDKDEVPQGLGFYNAVAIPCYTTLT-----QILPTEP 750  
 DB 740 FHEQGLEKTVLDDQPIPMMDRKAABLPCLQVGFIDPCTFYVKKFSRHEIILMPFR 799  
 QY 751 L-----LKACRDNINQWEKVIIRGETAMMISGPGAPBSKST 786  
 DB 800 LQNNRKEMKALADEYEKAKKALBEEKQQQEDRTTAKKAGTEICNGBPAPKST 852  
 RESULT 10  
 A36617  
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine  
 N/Alternate names: CGMP phosphodiesterase beta chain  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
 C/Accession: A36617; S19145; S14011; S00251  
 R/Lipkin, V.M.; Khramtsov, N.V.; Vasil'yevskaya, I.A.; Atabekova, N.V.; Muradov, K.G.; Gut  
 J. Biol. Chem. 265, 12955-12959, 1990  
 A/Title: Beta-subunit of bovine rod photoreceptor CGMP phosphodiesterase. Comparison with  
 A/Reference number: A36617; MUID:90330632; PMID:2165450  
 A/Accession: A36617  
 A/Molecule type: mRNA  
 A/Residues: 1-853 <LIP>  
 A/Cross-references: UNIPARC:P23439; UNIPARC:UPI0000127C2F; GB:J05553; NID:G162824; PIDN:  
 A/Experimental source: retina  
 A/Note: 40-AzG was also found  
 R/Lipkin, V.  
 submitted to the EMBL Data Library, December 1990  
 A/Reference number: S19145  
 A/Accession: S19145  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-853 <LIP>  
 A/Cross-references: UNIPARC:UPI0000127C2F; EMBL:X57146; NID:G209; PIDN:CAA40436.1; PID:G  
 R/Lipkin, V.M.; Gubanov, V.V.; Khramtsov, N.V.; Vasil'yevskaya, I.A.; Atabekova, N.V.; Mur  
 Biorg. Khim. 16, 118-120, 1990  
 A/Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the bet  
 A/Reference number: S14011; MUID:90267525; PMID:2161230  
 A/Accession: S14011  
 A/Status: preliminary  
 A/Molecule type: mRNA

A/Residues: 1-2,'P',4'-90,'P',92-93,'H',95-202,'VN',205-489,491-853 <LIP>  
 A/Cross-references: UNIPARC:UPI00001759BA; EMBL:X57146  
 R/Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.B.; I  
 FEBS Lett. 223, 169-173, 1987  
 A/Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpi  
 A/Reference number: S00161; MUID:88030033; PMID:2822478  
 A/Accession: S00251  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 534-536,'RRSNC',542-596,'Y',598-601,'W',603-606,'QLI' <OVC>  
 A/Cross-references: UNIPARC:UPI00001759BB  
 C/Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide ph  
 C/Keywords: acetylated amino end; blocked amino end; cGMP; cGMP binding; phosphoric diest  
 P:2-853/Product: 3',5'-cyclic-GMP phosphodiesterase beta chain #status predicted <MAT>  
 F:1556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 16.3%; Score 684; DB 2; Length 853;  
 Best Local Similarity 24.5%; Pred. No. 8-5e-43;  
 Matches 218; Conservative 152; Mismatches 354; Indels 164; Gaps 25;

QY 23 SLTDERKVAYSLSHPQVLDEFVSVAETVKMLKRTNKAQDPSKESRYQD---T 79  
 DB 2 SLSEGVHRFLDQNGFADQYFGRKLSPEQVA-----NACEGCGPFGTSPRLCOV 53  
 QY 80 NMQGVVYELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGAFALYFLGECNNSLCVFP 139  
 DB 54 EESALFELVQDMQEVNNERNVVFYKILRLCSILH---ADKCSLFMYQRN----- 101  
 QY 140 PGKKEGQPRILPAGP-----ITQGTTSAYVAKSRKTLVLEDILGDERP 183  
 DB 102 -GVAEIATPLTSVQDPSVLEDCLPVDSRIIVPLDIGVGVHVAQTKQVNVQDVMECPHF 160  
 QY 184 PRGTGLSESTRIGSVLCLPIYTAIGDLIGILLYRHWGEACLSHQEV-----ATAN 236  
 DB 161 SSGFADRLTYVRNLTATPIANG-KDVAVVIMAVNKLDPCEPTESEDEDFLYKYLEGTLN 219  
 QY 237 LMAASYA-IHQVOVCGRLAKQFELNDPILDSVKTYEDNVAIDSLSEHIMTYAKNLVND 295  
 DB 220 LKTYHLSTYLNCESTRG-----QVLLMSANKVFESLIDIERPHKAFYTVRAVLNCD 271  
 QY 296 RCALFQVDHKNKELYDLDLFDI-----GEE-----KEGKPIRK 327  
 DB 272 RYSVGLDMDTKKEKFEFDVMPVLNGEAQPSGPRTPGRIILFYKVIDYILHGKEDIKV 331  
 QY 328 KTKTEIRPSIEKGIAGQVARTGEVLNIPDAVADPRFN-REVDL- YGYTTRNIIICMPYV 384  
 DB 332 SPADHMAIASGLPTTVASGFIICNMTNAADEMTFTQGEPLDSDGVINQVLSMPTV 389  
 QY 385 RGSVIGVQVQWVKISGSASFSTDENNKMPAVFCALALHCANNYHRIHSECIYRVTM 444  
 DB 392 KEIRIVGATFYNNKDKGKPFDEQEVLMESLTQFLGMSVLTMTDFYDKNKKLENKIDIAQ 449  
 QY 445 LSHHSICTSEEWQGLM---RPNLPARICDIDILFPHDIDGPFENMWG---IFVYMH 497  
 DB 452 VLTVHRCDBEIQILPTFRERLKEKPADCEDELGIT-----LKEVLPGPSKFDIYEFH 507  
 QY 498 -----CGTSC-FEL-----EKLCPFMSYKQYRVRYNNMKAAVTVAH 535  
 DB 508 DLECTELKLVKCGIQMYTELGAVRKFOIPQEVLRVLFPSYSKGYRRIITYNNMRGFRV 567  
 QY 536 CMYAILQNN--NGLFTDLERKGLLIACLDHLDHGFNSNYLQKFDHPLAALYSTSTM 593  
 DB 568 TMFTLLMTGKLSKSYTDLDEAFAMVTAGLCCHDIDHRTNNLYQMSQNPPLAKHGSSIL 627  
 QY 594 HHHSQTVSIIQLGHNIFSTLSSEYQVLEIRKAIITADLALYFGNRKOLEMYOT 653  
 DB 628 HHHLEFGKFLSEETLNIYQNLNRQHSHVHIMDAIITADLALYFKKRTMFOKIVD--- 684  
 QY 654 LNLHNSHRDR-----VIGLMTACDLCSVTKLMPVTKLTANDIYAE 697  
 DB 685 -----ESKNYEDRKSNWEYLSLETRKEIIVMMAMMTACDLSATKMEVQSKVALLVALE 741









FEBS Lett. 223, 169-173, 1987  
 A>Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha  
 A/Accession: S00161; MUID:88030033; PMID:2822478  
 A/Molecule type: mRNA  
 A/Residues: 1-859 <CNP>  
 A/Cross-references: UNIPARC:UPI000016C2D7; EMBL:M27541; NID:q162826; PIDN:AAA30441.1; PI  
 A/Note: part of this sequence was confirmed by protein sequencing  
 A/Note: 381-Val was also found  
 R/Pitler, S.U.; Behr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTunen, R.  
 Genomics 6, 272-283, 1990  
 A>Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi  
 A/Reference number: A34611; MUID:90169986; PMID:2155175  
 A/Accession: A34611  
 A/Molecule type: mRNA  
 A/Residues: 1-193, 'V', 195-423, 'T', 425-674, 'F', 676-859 <PIT>  
 A/Cross-references: UNIPARC:UPI000016C2D8; GB:M26043; NID:q162833; PIDN:AAA30443.1; PID:  
 C/Comment: This protein is involved in the transduction and amplification of the visual  
 C/Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P  
 C/Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; ret  
 F/2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <CN  
 F/558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
 F/2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 15.8%; Score 666.5; DB 1; Length 859;  
 Best Local Similarity 25.0%; Pred. No. 1,8e-41;  
 Matches 210; Conservative 144; Mismatches 348; Indels 139; Gaps 20;

48 VSAETVEKMLKRTKTKAK-----DESPKREV---SKYQDTNM---QGVYVE 87  
 4 VTAAEVEKFLDSNVSPFAQYVNLRYRAKVISDLPLPREAAVDFSNVHALNSVESEIIFD 63  
 88 LNSYIEQGLDTGSDNHLLEYLSIIIRATKADGFPALYLGECSNLSLCTFIPRKGEGP 147  
 64 LIRDFQDNLQA---EKCVFNVKKLCELLQDRMSLFMYTRRN-----GIAELAT 110  
 148 RLIPAG-----PIQGTTSAAVYAKSKRTLLVEDILGDERFPRGTGL 189  
 111 RLFNHKAVALBECVAADSEIVPFLDMG--VGVHVALSKITVNPVPTREDDHFCDFVDT 168  
 190 ESGTRIGQVLCPIVTAIGDLIGILELYHMKGEAFCLSHQEAATAMASVA----- 243  
 169 LTBVQTKNIIASPIWNG-KDVVAIIMAVNVKVDGPHTEDEBEILLKYLANFANLIMKVFHL 227  
 244 --IHQVQCRGLAKQTELDNPLLDVSKTYFDNIIVADLSLEHIMITYAKNLVNAIDCALFQ 301  
 228 SYLHNCESTRRG-----QILLMSGKVFEELTDIERQFHAKLYTVRAFLNCDHRSVGL 279  
 302 VDHKKKELYSDFDI-----GEE-----KEGKPIFKTKKEIR 333  
 280 LDMTKQKEFPDVPVPLMGEPAPRYAPRPDGRINPYKVIDIILHGKEDIKYIPRPPRH 339  
 334 FSIIEGIAQVARTGEVLTINIPDAVDP--RFRREVDTLYGTTRNIIICMPIVS-RGSVIG 390  
 340 WALVAGLPTVVAQNGLICINIMAPSEDFPAFOKEPLDESGMMIKVLSMPVYNKKEEIIYG 399  
 331 VVQVMNKSIGSASFSTDENNFQMPAVFCAALAHCAANNYRIHSHSICITYVMMEKSYHSI 450  
 400 VATFNRRDQKFPDEMDETLMESLAQFLGMSVLANPDTYELMKNLEKRRKIDFODMKYHNK 459  
 451 CTSEEMOGIMRF-----NLPARICRDIIEFHFDIOP---FENN 485  
 460 CDNEIQTITLKREYVYGKEPWECEBELAELLQGLPRADKYKELNFKHSDFPLRELEIV 519  
 486 WPIGFVYMIHRSCTSCPELEKLCRFINSVKKNYRVRPYNHKKAAVTAACHQVAILQNN- 544  
 520 KCGIGMYTELKVVDPKPHIQEALVRFMYSLSKGYRRIITYHNMRHGFNVQGTFFSLLVGK 579  
 545 -NGLEFTEERKULLAACLCHDDHNGFSNSYLOKQDHPALALYSTSTMEQHHPQSQTSL 603  
 580 LKRYPTDEALAMVTAAFCHDIDHGTNNMLYQMSQNPPLAKLHGSSILERRHLEFGKTL 639  
 604 QLEGNITSTLSSSEVQGLERIRKAIATDIALVFGNKKQLEEM-----YQT-----GS 653

DB RDESLNITQNLNRRQHEHAHMMODIAITATDLATYCKKRTMFOKIVDSKTYETQGEWTQ 699  
 640 LNLNQHSHRDYVIGLMTATCULCSVTKMPYTKLTANDIYAFNAEGD-EMKGGIGIQTIP 712  
 654 LNLNQHSHRDYVIGLMTATCULCSVTKMPYTKLTANDIYAFNAEGD-EMKGGIGIQTIP 712  
 700 YMMLDQTKKEIYVMMAMMTACDLISATTKPWEQSKVALLVAEPFEGDLERTVLAQNPFP 759  
 723 MMDRDKREVEQOGQGFNAVAIPCYTTLTGQILPTEPELTKACRDNLQWEKVIIRGEETA 772  
 760 MMDRDKADELKLQVGFIDFCTFYKKEFSRFBHEITFMIDGITNNRKEMKALADYEYTK 819  
 773 M 773  
 DB 820 M 820

RESULT 15  
 B34611  
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 21-Jan-2000  
 C/Accession: B34611  
 R/Pitler, S.U.; Behr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTunen, I  
 Genomics 6, 272-283, 1990  
 A>Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodie  
 A/Reference number: A34611; MUID:90169986; PMID:2155175  
 A/Accession: B34611  
 A/Status: Preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-859 <PIT>  
 A/Cross-references: UNIPARC:UPI00001759B9; GB:M26061  
 C/Genetics:  
 A/Gene: GDB:PDE6A; PDEA  
 A/Cross-references: GDB:120265; OMIM:180071  
 A/Map position: sq1.2-5q34  
 C/Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p  
 C/Keywords: cGMP binding; phosphoric diester hydrolase  
 F/558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 15.8%; Score 663.5; DB 2; Length 859;  
 Best Local Similarity 24.8%; Pred. No. 3e-41;  
 Matches 208; Conservative 138; Mismatches 338; Indels 155; Gaps 21;

48 VSAETVEKMLKRTKTKAKD-----BSPKREVRYQDT 79  
 4 VTAAEVEKFLDSNVSPFAQYVNLRYRAKVISDLGAKAAVDFSNVHSPSSMBSE----- 59  
 80 NMQGVYELNSYIEQRLDTGSDNHLLEYLSIIIRATKADGFPALYLGECSNLSLCTFIP 139  
 60 ----IIFDLDFQENIQT---EKCFNVKKLCELLQDRMSLFMYTRRN----- 103  
 140 PQMKEGQRLIPAG-----PIQGTTSAAVYAKSKRTLLVEDILGDE 181  
 104 -GIAELATRLFNHKAVALBECVAADSEIVPFLDMG--VGVHVALSKITVNPVPTREDE 160  
 182 RFRPGTGESGTRIGQVLCPIVTAIGDLIGILELYR---HMKG--EAFCLSHQEAAT 234  
 161 HFCDVVDILTETKTKNIIASPIWNG-KDVVAIIMAVNVKVDGSHFKRBEILLKTLNFRAN 219  
 235 ANLAWASVA-IHQVQCRGLAKQTELDNPLLDVSKTYFDNIIVADLSLEHIMITYAKNLVN 293  
 220 LIMKVVHLSYLNCESTRRG-----QILLMSGKVFEELTDIERQFHAKLYTVRAFLN 271  
 294 ADRCALPQVDHKKNELYSDFDI-----GEE-----KEGKPI 325  
 272 CDRSISVGLDMTKQKEFPDVPVPLMGEPVPSGPRPDGRINPYKVIDIILHGKEDIKV 331  
 326 FKTKKEIRFSIEKGIAGQVARTGEVLTINIPDAVDP--RFRREVDTLYGTTRNIIICMPIV 383  
 332 IPNPPDHMALVSGLPTVVAQNGLICINIMAPSEDFPAFOKEPLDESGMMIKVLSMPV 391  
 384 S-RGSVIGVQVMVKNKISGASFSTDENNFQMPAVFCAALAHCAANNYRIHSHSICITYVM 442



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Db      61 TNKADBPSPKESVSHRYODTNMGVVYELNSYIEQRLDITGDNHLLLYELSSIIIRIATYAD 120
Qy      121 GFALYFLGECNNSLCVFPIPGMKEGQPRLLIPAGPIITGTTISAVYAKSRKTLVIEDIIGD 180
Db      121 GFALYFLGECNNSLCVFPIPGMKEGQPRLLIPAGPIITGTTISAVYAKSRKTLVIEDIIGD 180
Qy      181 ERFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHOEVAATANLAMA 240
Db      181 ERFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHOEVAATANLAMA 240
Qy      241 SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNNYVALDSLHEIMITYAKNLVNAARCALF 300
Db      241 SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNNYVALDSLHEIMITYAKNLVNAARCALF 300
Qy      301 QVDHNKELYSDFPIGEEKGKPIPKTKKEIRFSIKGIAGVARTGVLTNPDAVADP 360
Db      301 QVDHNKELYSDFPIGEEKGKPIPKTKKEIRFSIKGIAGVARTGVLTNPDAVADP 360
Qy      361 RFRNEVDLYGTYTTNNILCMPIVSRGSYIGVQVWNKISGSAFSKTDENNFMFAVFCAL 420
Db      361 RFRNEVDLYGTYTTNNILCMPIVSRGSYIGVQVWNKISGSAFSKTDENNFMFAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVPHNMKGAVTVACHYAI 540
Db      481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVPHNMKGAVTVACHYAI 540
Qy      541 LQNNNGFLTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTSTMEQHHFSQTV 600
Db      541 LQNNNGFLTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTSTMEQHHFSQTV 600
Qy      601 SILOEGHNISTSSSEYEOVLLEIRKAIITDIALYFGNRKOIEMVQTSGLNLHNS 660
Db      601 SILOEGHNISTSSSEYEOVLLEIRKAIITDIALYFGNRKOIEMVQTSGLNLHNS 660
Qy      661 HRDRVIGLMTACDLCSTYKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Db      661 HRDRVIGLMTACDLCSTYKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Qy      721 EVPOGOLGFYNAVALPCYTTTLTQILPTEPELAKACRDNLQWEKVIKGEETAMVISCGRP 780
Db      721 EVPOGOLGFYNAVALPCYTTTLTQILPTEPELAKACRDNLQWEKVIKGEETAMVISCGRP 780
Qy      781 APSKSTPEKLVKVED 796
Db      781 APSKSTPEKLVKVED 796

RESULT 2
QyOyDb RAT PRELIMINARY; PRT; 794 AA.
AC QOYJ6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
DE PDE10A2 (EC 3.1.4.17).
GN Name=Pde10a; Synonyms=PDE10A;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=SD; TISSUE=Brain;
RX MEDLINE=20050627; PubMed=10583409;
RA Fujishige K., Kozera J., Omori K.;
RT "Striatal and testis-specific phosphodiesterase PDE10A: isolation and
RT characterization of a rat PDE10A.";
RL Eur. J. Biochem. 266:1118-1127(1999).

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DR EMBL; AB027155; BAA68996.1; -; mRNA.
DR Ensembl; ENSRNOC00000011310; Rattus norvegicus.
DR RGD; 68434; Pde10a.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:007165; F:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDbase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDbase_I; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM0065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDbase_I; 1.
KW Hydrolyase.
SQ
SEQUENCE 794 AA; 90161 MW; A36C4678B385846E CRC64;

Query Match          98.0%; Score 4123; DB 2; Length 794;
Best Local Similarity 98.4%; Pred. No. 5.6e-310;
Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy      1 MEDPSNNASCFRRLTEGFLSPSLTDEKVAIYSLHQVYVDEPFSSEVSATVEKWKRRK 60
Db      1 MEDPSNNASCFRRLTEGFLSPSLTDEKVAIYSLHQVYVDEPFSSEVSATVEKWKRRK 60
Qy      61 TNKADBPSPKESVSHRYODTNMGVVYELNSYIEQRLDITGDNHLLLYELSSIIIRIATYAD 120
Db      61 TNKADBPSPKESVSHRYODTNMGVVYELNSYIEQRLDITGDNHLLLYELSSIIIRIATYAD 120
Qy      121 GFALYFLGECNNSLCVFPIPGMKEGQPRLLIPAGPIITGTTISAVYAKSRKTLVIEDIIGD 180
Db      121 GFALYFLGECNNSLCVFPIPGMKEGQPRLLIPAGPIITGTTISAVYAKSRKTLVIEDIIGD 180
Qy      181 ERFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHOEVAATANLAMA 240
Db      181 ERFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHOEVAATANLAMA 240
Qy      241 SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNNYVALDSLHEIMITYAKNLVNAARCALF 300
Db      241 SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNNYVALDSLHEIMITYAKNLVNAARCALF 300
Qy      301 QVDHNKELYSDFPIGEEKGKPIPKTKKEIRFSIKGIAGVARTGVLTNPDAVADP 360
Db      301 QVDHNKELYSDFPIGEEKGKPIPKTKKEIRFSIKGIAGVARTGVLTNPDAVADP 360
Qy      361 RFRNEVDLYGTYTTNNILCMPIVSRGSYIGVQVWNKISGSAFSKTDENNFMFAVFCAL 420
Db      361 RFRNEVDLYGTYTTNNILCMPIVSRGSYIGVQVWNKISGSAFSKTDENNFMFAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVPHNMKGAVTVACHYAI 540
Db      481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVPHNMKGAVTVACHYAI 540
Qy      541 LQNNNGFLTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTSTMEQHHFSQTV 600
Db      541 LQNNNGFLTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTSTMEQHHFSQTV 600
Qy      601 SILOEGHNISTSSSEYEOVLLEIRKAIITDIALYFGNRKOIEMVQTSGLNLHNS 660
Db      601 SILOEGHNISTSSSEYEOVLLEIRKAIITDIALYFGNRKOIEMVQTSGLNLHNS 660
Qy      661 HRDRVIGLMTACDLCSTYKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Db      661 HRDRVIGLMTACDLCSTYKLMPTVKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Qy      721 EVPOGOLGFYNAVALPCYTTTLTQILPTEPELAKACRDNLQWEKVIKGEETAMVISCGRP 780
Db      721 EVPOGOLGFYNAVALPCYTTTLTQILPTEPELAKACRDNLQWEKVIKGEETAMVISCGRP 780

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QY 781 APSKSTPEKLVKVED 796  
DB 779 ATSKSTSEKTRKVD 794

## RESULT 3

QTPG2 MOUSE PRELIMINARY; PRT; 797 AA.

DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Pdel10a.  
GN Name=Pdel10a Mus musculus;  
OS Mus musculus (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RA Li S., Tian R., Bratwaite M., Waeltz P., Nagaraja R., Roe B.A.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC104323; AAP94049.1; -; Genomic DNA.  
DR GO; GO:0004114; F.3', 5'-cyclic-nucleotide phosphodiesterase a. .; IEA.  
DR GO; GO:0016787; P:hydrolyase activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDBase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PR00333; PDBase\_I; 1.  
DR PRINTS; PR00387; PDISTERASBL.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDASE\_I; 1.  
SQ SEQUENCE 797 AA; 90275 MW; BEB1442A95131C8A CRC64;

Query Match 97.2%; Score 4089.5; DB 2; Length 797;

Best local Similarity 98.2%; Pred. No. 2.2e-307;

Matches 778; Conservative 2; Mismatches 5; Indels 7; Gaps 1;

QY 12 PRLTSCPLSPS-----LTDEKVAAYLSLHPQVLDSEVSASAEYKMKRKTNKA 64  
DB 6 PQQAQCLCFPPSPSATTGTLTDEKVAAYLSLHPQVLDSEVSASAEYKMKRKTNKA 65  
QY 65 KQEPSEKVSRYQDTMVGAVYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGPA 124  
DB 66 KQEPSEKVSRYQDTMVGAVYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGPA 125  
QY 125 YFDEGCNNSLCVTPIPKMEGQRLIPAGITGGTTSATVAASRKLVLVEDLIGDERFP 184  
DB 126 YFDEGCNNSLCVTPIPKMEGQRLIPAGITGGTTSATVAASRKLVLVEDLIGDERFP 185  
QY 185 RRGGLSGTRIGSVLCPIYTAIGDLIGILELYRMGKEAFCSHOEVATANTAMASVAI 244  
DB 186 RRGGLSGTRIGSVLCPIYTAIGDLIGILELYRMGKEAFCSHOEVATANTAMASVAI 245  
QY 245 HQVQVGRGLAKQTELDPLDVSXTYFDNIVAIDSLLEHIMYAKNLVNDRCALFQVDH 304  
DB 246 HQVQVGRGLAKQTELDPLDVSXTYFDNIVAIDSLLEHIMYAKNLVNDRCALFQVDH 305  
QY 305 KKKELYSDFLDIGBEKSGKPIFKKTKKIRPSIEKIGAGVARGENTINIDADPPENR 364  
DB 306 KKKELYSDFLDIGBEKSGKPIFKKTKKIRPSIEKIGAGVARGENTINIDADPPENR 365  
QY 365 EVDLYGYTRNLLCMPIVRSVYIGVAVVQVWVKNKISSAFSKTDENNKKMFVFCALALHC 424  
DB 366 EVDLYGYTRNLLCMPIVRSVYIGVAVVQVWVKNKISSAFSKTDENNKKMFVFCALALHC 425  
QY 425 ANMYHRIHSECIYRVTMKLSYHSICTSEWQGLMFLNLPARICRDIELFHPDIGPEN 484

DB 426 ANMYHRIHSECIYRVTMKLSYHSICTSEWQGLMFLNLPARICRDIELFHPDIGPEN 485

QY 485 MPPGIFVTMIHRSCTSCFELEKLCRFIMSYKYNRRVPYNNMKAATVAICMTAIIQNN 544

DB 486 MPPGIFVTMIHRSCTSCFELEKLCRFIMSYKYNRRVPYNNMKAATVAICMTAIIQNN 545

QY 545 NGLFTDLERKGLIATCLCHDDHREGSNSYLQKPDHPALAYSTSTMEQHFPSQTVSIIQ 604

DB 546 NGLFTDLERKGLIATCLCHDDHREGSNSYLQKPDHPALAYSTSTMEQHFPSQTVSIIQ 605

QY 605 LEGHNIFFSTLSSSEYQVLEIRKAIINTDLALYGNRKQLEBMYQTSGLNIHQSHDR 664

DB 606 LEGHNIFFSTLSSSEYQVLEIRKAIINTDLALYGNRKQLEBMYQTSGLNIHQSHDR 665

QY 665 VIGLMTACDLCSYTKLMPYTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXDEVQ 724

DB 666 VIGLMTACDLCSYTKLMPYTKLTANDIYAEFMAEGDEMKLGIOPIPMDDKXDEVQ 725

QY 725 GOLGFYNAVAIPCYTTLQIILPTEPLKACRDINOMEKVIRGETAMWISGPPAPSK 784

DB 726 GOLGFYNAVAIPCYTTLQIILPTEPLKACRDINOMEKVIRGETAMWISGPPAPSK 785

QY 785 STEPKLVKVED 796

DB 786 STEPKLVKVED 797

## RESULT 4

QTPG1 MOUSE PRELIMINARY; PRT; 773 AA.

AC QTPG1;  
DT 01-OCT-2003 (Tremblrel. 25, Created)  
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Pdel10a (Fragment).  
GN Name=Pdel10a Mus musculus;  
OS Mus musculus (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RA Li S., Tian R., Bratwaite M., Waeltz P., Nagaraja R., Roe B.A.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC104323; AAP94050.1; -; Genomic DNA.  
DR GO; GO:0004114; F.3', 5'-cyclic-nucleotide phosphodiesterase a. .; IEA.  
DR GO; GO:0016787; P:hydrolyase activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDBase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PR00333; PDBase\_I; 1.  
DR PRINTS; PR00387; PDISTERASBL.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDASE\_I; 1.  
FT NON\_TER 1  
SQ SEQUENCE 773 AA; 87794 MW; 0C0E353B72940912 CRC64;

Query Match 97.0%; Score 4080; DB 2; Length 773;

Best local Similarity 100.0%; Pred. No. 1.2e-306;

Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LTDEKVAAYLSLHPQVLDSEVSASAEYKMKRKTNKADEBPKVSRYQDTMVG 83  
DB 1 LTDEKVAAYLSLHPQVLDSEVSASAEYKMKRKTNKADEBPKVSRYQDTMVG 60  
QY 84 VYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGPAFLYFDEGCNNSLCVPIPGMK 143

D	b	61	VYELNSYIEQRLDTGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIPGK 120
Q	y	144	EGQPLIPAGPIITGGTTISAVYAKSRKTLVIEDILGDEFPFGTGLSESTRIQSVLCPI 203
D	b	121	EQQPLIPAGPIITGGTTISAVYAKSRKTLVIEDILGDEFPFGTGLSESTRIQSVLCPI 180
Q	y	204	VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 263
D	b	181	VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 240
Q	y	264	LDVSKTYEDNIVAIIDSLLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 323
D	b	241	LDVSKTYEDNIVAIIDSLLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 300
Q	y	324	PIFKTKIEIRSEIEKGIAGQVARTGEVLNIPDAYADPRNREVDLYTGTTRNIIICMPIV 383
D	b	301	PIFKTKIEIRSEIEKGIAGQVARTGEVLNIPDAYADPRNREVDLYTGTTRNIIICMPIV 360
Q	y	384	SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTME 443
D	b	361	SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTME 420
Q	y	444	KLSTHSICTSEEMOGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 503
D	b	421	KLSTHSICTSEEMOGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 480
Q	y	504	ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAIIQNNNGLPFDLERKGLIACCH 563
D	b	481	ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAIIQNNNGLPFDLERKGLIACCH 540
Q	y	564	DLDRHGFNSYIQKFDHPALALYSTSTMEQHHFSGQVSILOLEGHNIFSTLSSSEYQVL 623
D	b	541	DLDRHGFNSYIQKFDHPALALYSTSTMEQHHFSGQVSILOLEGHNIFSTLSSSEYQVL 600
Q	y	624	EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDVIIGLMTACDLCSTYKLM 683
D	b	601	EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDVIIGLMTACDLCSTYKLM 660
Q	y	664	VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQQLGFYNAVAIPCTTTTLTQ 743
D	b	661	VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQQLGFYNAVAIPCTTTTLTQ 720
Q	y	744	ILPTEPLILKACRDNLNOMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 796
D	b	721	ILPTEPLILKACRDNLNOMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 773
RESULT 5			
09WV11_MOUSE PRELIMINARY; prt; 779 AA.			
AC	09WV11	01-NOV-1999	(TrEMBLrel. 12, Created)
DT	01-NOV-1999	(TrEMBLrel. 12, last sequence update)	
DR	01-MAR-2004	(TrEMBLrel. 26, last annotation update)	
DE	CAMP/cGMP phosphodiesterase.		
OS	Name=Pde10a;		
ON	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
NC	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISUS=Testis;		
RA	MEDLINE=99289599; PubMed=10359840; DOI=10.1073/pnas.96.12.7071;		
RT	Soderling S.H., Bayuga S.J., Beavo J.A.;		
RT	"Isolation and characterization of a dual-substrate phosphodiesterase		
RT	gene family: PDE10A.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 96:7071-7076(1999).		
DR	EMBL; AF110507; AAD31544.1; -; mRNA.		
DR	Ensembl; ENSMUSG0000023868; Mus musculus.		
DR	MGI; MGI:1345143; Pde10a.		
DR	GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IDA.		

DR	InterPro; IPR003018; GAF.		
DR	InterPro; IPR003607; Met_phos_hydro.		
DR	InterPro; IPR002073; PDEase.		
DR	Pfam; PF01590; GAF; 2.		
DR	Pfam; PF00233; PDEase_1; 1.		
DR	PRINTS; PR00387; PDIESTERASE1.		
DR	SMART; SM0065; GAF; 2.		
DR	SMART; SM00471; HDC; 1.		
DR	PROSITE; PS00126; PDEASE_1; 1.		
SQ	SEQUENCE 779 AA; 88516 MW; 83691872PDDEEAB CRC64;		
Query Match			
Best Local Similarity 100.0%; Score 4080; DB 2; Length 779;			
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	24	LTDENVKAYLSLHPQVLDPEFVSESATVTEKMLKRTKNKAKDESPREVSRYQDTNNQ	83
D	7	LTDENVKAYLSLHPQVLDPEFVSESATVTEKMLKRTKNKAKDESPREVSRYQDTNNQ	66
Qy	84	VYELNSYIEQRLDTGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIPGK	143
D	67	VYELNSYIEQRLDTGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIPGK	126
Qy	144	EGQPLIPAGPIITGGTTISAVYAKSRKTLVIEDILGDEFPFGTGLSESTRIQSVLCPI	203
D	127	EGQPLIPAGPIITGGTTISAVYAKSRKTLVIEDILGDEFPFGTGLSESTRIQSVLCPI	186
Qy	204	VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL	263
D	187	VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL	246
Qy	264	LDVSKTYEDNIVAIIDSLLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK	323
D	247	LDVSKTYEDNIVAIIDSLLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK	306
Qy	324	PIFKTKIEIRSEIEKGIAGQVARTGEVLNIPDAYADPRNREVDLYTGTTRNIIICMPIV	383
D	307	PIFKTKIEIRSEIEKGIAGQVARTGEVLNIPDAYADPRNREVDLYTGTTRNIIICMPIV	366
Qy	384	SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTME	443
D	367	SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTME	426
Qy	444	KLSTHSICTSEEMOGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF	503
D	427	KLSTHSICTSEEMOGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF	486
Qy	504	ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAIIQNNNGLPFDLERKGLIACCH	563
D	487	ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAIIQNNNGLPFDLERKGLIACCH	546
Qy	564	DLDRHGFNSYIQKFDHPALALYSTSTMEQHHFSGQVSILOLEGHNIFSTLSSSEYQVL	623
D	547	DLDRHGFNSYIQKFDHPALALYSTSTMEQHHFSGQVSILOLEGHNIFSTLSSSEYQVL	606
Qy	624	EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDVIIGLMTACDLCSTYKLM	683
D	607	EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDVIIGLMTACDLCSTYKLM	666
Qy	664	VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQQLGFYNAVAIPCTTTTLTQ	743
D	667	VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQQLGFYNAVAIPCTTTTLTQ	726
Qy	744	ILPTEPLILKACRDNLNOMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED	796
D	727	ILPTEPLILKACRDNLNOMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED	779
RESULT 6			
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ID	Q8CA95		
AC	Q8CA95		
DT	01-MAR-2003	(TrEMBLrel. 23, Created)	

01-MAR-2003 (TRENBLER). 23, last sequence update)  
 01-MAR-2004 (TRENBLER). 26, last annotation update)  
 Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A33007P15 product:phosphodiesterase 10A, full insert sequence.  
 GN Name:Pde10a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
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 NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RM MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Meth. Enzymol. 303:19-44(1999).  
 (2)  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RC MEDLINE=21085560; PubMed=11217651; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann M., Gaasterland T., Gissi C., King B., Kochiwa H., Kuenh P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J., Schmitt L.M., Stabli P., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guestinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbetsu P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Williams L., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohnauki S., Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 (3)  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RC The PANTOM Consortium;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 (4)  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RM MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 (5)  
 NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kikunishi T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-364-format sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).

[6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal cord;  
 RA Adachi J., Aizawa K., Akiyama T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hasegawa T., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozawa T., Hori F., Imotani K., Ishii Y., Itoh M., Kondo S., Kono H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Nakamura M., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okazaki Y., Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Yasunishi M., Hayashizaki Y.;  
 RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK039249; BAC30292.1; -; mRNA.  
 DR Ensembl; ENSMUSG000000238668; Mus musculus.  
 DR MGI; MGI:1345143; Pde10a.  
 DR GO; GO:0004114; F.3',5'-cyclic-nucleotide phosphodiesterase a. .; IDA.  
 DR InterPro; IPR003018; GAF.  
 DR InterPro; IPR003607; Met\_phos\_hydro.  
 DR InterPro; IPR02073; PDbase.  
 DR Pfam; PF01590; GAF; 2.  
 DR Pfam; PR00387; PDbase; 1.  
 DR SMART; SM00065; GAF; 2.  
 DR SMART; SM00471; HDC; 1.  
 DR SMART; PS00126; PDEASB; 1.  
 DR SEQUENCE 790 AA; 89438 MW; 1AC6F11A5AD7B92 CRC64;  
 Query Match 96.8%; Score 4072; DB 2; Length 790;  
 Best Local Similarity 99.9%; Pred. No. 5e-306; 1; Indels 0; Gaps 0;  
 Matches 772; Conservative  
 24 LIDDEKAVATSLHPQVLDSEVSASAEVETKMLRKTKAKADESPKVSRYQDTNMG 83  
 18 LIDDEKAVATSLHPQVLDSEVSASAEVETKMLRKTKAKADESPKVSRYQDTNMG 77  
 84 VYIEINLSYIEQRLDTGCDNHLILYELSSIRATKADGALYFLGECNNSLCYFIPRGM 143  
 78 VYIEINLSYIEQRLDTGCDNHLILYELSSIRATKADGALYFLGECNNSLCYFIPRGM 137  
 144 EGQPRILPAGPIPTGCTTISAVYAKSKTLLVEDIIGDESPFGTSGESGRISQVCLPI 203  
 138 EGQPRILPAGPIPTGCTTISAVYAKSKTLLVEDIIGDESPFGTSGESGRISQVCLPI 197  
 204 VTAIGDLIGLIELYRMGKEAFCLSHQEVATANIWASVALIHQVYCRGLAKQTEINDFL 263  
 198 VTAIGDLIGLIELYRMGKEAFCLSHQEVATANIWASVALIHQVYCRGLAKQTEINDFL 257  
 264 LDVSKTYPDNIVALIDLEHIMIVANLVNADRCALFOVDHKNKELYSDFDGEKEGK 323  
 258 LDVSKTYPDNIVALIDLEHIMIVANLVNADRCALFOVDHKNKELYSDFDGEKEGK 317  
 324 PIFKTKETKEIRFSEKGIQAQVARTGVANIPDAVADPRFREVDTLYGTYTRNIIICMPIV 383  
 318 PIFKTKETKEIRFSEKGIQAQVARTGVANIPDAVADPRFREVDTLYGTYTRNIIICMPIV 377  
 384 SRGSVTIGVQWVWKISGSAFSKTDENPFKMAFVFCALALHLCAMRYIRHSECIYVTME 443  
 378 SRGSVTIGVQWVWKISGSAFSKTDENPFKMAFVFCALALHLCAMRYIRHSECIYVTME 437  
 444 KLSYHSICTSEEWQGLMFRPLPARICRDIELFPHDIGPEENWPGIFVTMIHRSCTSCF 503  
 438 KLSYHSICTSEEWQGLMFRPLPARICRDIELFPHDIGPEENWPGIFVTMIHRSCTSCF 497  
 504 ELEKLCRFPTMSYQKQRRVPYHNMKAAVVAHGMVAILLNNNGLFTDLERKGLIACLC 563  
 498 ELEKLCRFPTMSYQKQRRVPYHNMKAAVVAHGMVAILLNNNGLFTDLERKGLIACLC 557  
 564 DLDRGFSNSYLQKFDHPLAALYSTSTMEQHHSQVTSILQLEGHNIFFSTLSSESEYQVL 623  
 558 DLDRGFSNSYLQKFDHPLAALYSTSTMEQHHSQVTSILQLEGHNIFFSTLSSESEYQVL 617

Oy	624	ZIIRKAIITADUALYFGNRKQLEENYQTGSLNLHNSHDRITIGLMTACDLCSTYTKLP	683
Dd	618	EIRRAIIATDALYFNGRKQLSEENVQTGSINLHNQSHDRIVGLMMPACDLCSTYTKLP	677
Oy	684	VTKLTANDIYAEFMAGEDEMKKLGIPTIPMDRDKADEVPQGOLGFYNVAIIPCYYTLTQ	743
Dd	678	VTKLTANDIYAEFMAGEDEMKKLGIPTIPMDRDGRDEVPPQOLGFYNVAIIPCYYTLTQ	737
Oy	744	IILPPEPLIKACRDNIQNWEKVIRGEETAMWISGGPAPSKSTPEKLVNKVED	796
Dd	738	IILPPEPLIKACRDNIQNWEKVIRGEETAMWISGGPAPSKSTPEKLVNKVED	790
 RESULT 7 Q9ULW9_HUMAN PRELIMINARY; PRT; 789 AA.			
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AC	Q9ULW9_		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
DS	3',5'-cyclic nucleotide phosphodiesterase 10A2.		
GN	Name=PDE10A2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Fetal lung;		
RX	MEDLINE=99373117; PubMed=10441464; DOI=10.1006/brcr.1999.1013;		
RA	Korea J., Fujishige K., Yuasa K., Onori K.;		
RT	*Characterization and phosphorylation of pde10a2, a novel alternative		
RT	splice variant of human phosphodiesterase that hydrolyzes cAMP and		
RL	cGMP."		
RF	Biochem. Biophys. Res. Commun. 261:551-557(1999).		
DR	EMBL; AB026816; BA84467.1; -: mRNA.		
DR	GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.		
DR	GO; GO:0016787; F:hydrolyase activity; IEA.		
DR	InterPro; IPR003018; GAF.		
DR	InterPro; IPR003607; Met_phos_hydro.		
DR	InterPro; IPR002073; PDbase.		
DR	Pfam; PF01590; GAF; 2.		
DR	Pfam; PF00233; PDbase_I. 1		
DR	PRINTS; PR00387; PDJESTERASE1.		
DR	SMART; SMO0065; GAF; 2.		
DR	SMART; SMO0471; HGC; 1.		
DR	PROSITE; PS00126; PDASE_I; 1.		
SO	SEQUENCE 789 AA; 89385 MW; 7CC35F16735FB3C2 CRC64;		
 Query Match 95.2%; Score 4004; DB 2; Length 789; Best Local Similarity 95.6%; Pred. No. 9.2e-301; Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;			
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Dd	1	MEDGPSNNASGCFRRLLTECEFLSPSLTDEKVKAYLSLHPVLDEFESYSAAETVEKMLKKR	60
Oy	61	TNKADEBSPKEVSRKYODTNMGVVYLEINSYIEORLDTGSDNHLLLYELSSIIIRIATRAD	120
Dd	61	NNKSDESBAPKEVSRYODTNMGVVYLEINSYIEORLDTGSDNQLLLYELSSIIKIATRAD	120
Oy	121	GFAIFYFLGECNNSLCVFTIPPGKKEQQPLLIPAGPIITOGTTISAYYAASKRTLIVEDIIGD	180
Dd	121	GFAIFYFLGECNNSLCIFTTPPGIKKEKPRLLIPAGPIITOGTTISAVYAASKRTLIVEDIIGD	180
Oy	181	ERPFRGTLESSTRIQSVALCPITYVAIGDLGITELHYRWGKEAFCISHOEVAATNLMWA	240
Dd	181	ERPFRGTLESSTRIQSVALCPITYVAIGDLGITELHYRWGKEAFCISHOEVAATNLMWA	240
Oy	241	SVAIHQGVCGKLGAKQTELNDNFLDVSKTYPDNIYVAIDSLLEHMIVYAKNLVNADRCAF	300

Dd		241	SVATHQVOCRLAQTLENDLILDVSKTYFPIYVAIDBLEHIMYYAKVLVADKCALF	3000
Qy		301	QVDHNKKELYSDLPDIGEKEGKPIFKTKTEIRFSIEKGIAQAVATGEVLNIPDAVADP	3600
Dd		301	QVDHNKKELYSDLPDIGEKEGKPVFKTKTEIRFSIEKGIAQAVATGEVLNIPDAVADP	3660
Qy		361	RFRNEVDI.YTGYTTNNILCMP.VYSNGSYGVGMNQNKISGSASFSTDENNPFCAVFCL	4200
Dd		361	RFRNEVDI.YTGYTTNNILCMP.VYSNGSYGVGMNQNKISGSASFSTDENNPFCAVFCL	4260
Qy		421	ALHGANNMHTIRHSCEICRYVTMEKLSYHSICTSEEMOGLMRFNLPARCRDIELFFPDIG	4800
Dd		421	ALHGANNMHTIRHSCEICRYVTMEKLSYHSICTSEEMOGLMQTLTPVRLCKEILEFFPDIG	4860
Qy		481	PFEENMPGIFVYMHIRSGCGTSCFELEKL.CRFIMS.VKKNRYRVPYNMKKAIVTAHCMYA	5400
Dd		481	PFEENMPGIFVYMHIRSGCGTSCFELEKL.CRFIMS.VKKNRYRVPYNMKKAIVTAHCMYA	5460
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Dd		541	LONNNGLETDLERKGLLIACLCHDD.DHRGFNSYLQKFPHPLAALYSTSTMEQHNSQTV	6060
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Dd		601	SITOLEGNISTSSSEYBOYLEIIRKAIINTDALYPGNRKOLBEMV.QTSGLNHOS	6660
Qy		661	HDRVI.GLMNTACDLC.SVTKLMPVKLTANDIYAEFWAGDEMKLGIOPIPMDRDKD	7200
Dd		661	HRDRI.GLMNTACDLC.SVTKLMPVKLTANDIYAEFWAGDEMKLGIOPIPMDRDKD	7260
Qy		721	EVPQGQLGFYNAVAIPCCTTLTLQII.LPPEPLLKACRDNI.NQWEEKYIRGETAMWISGPB	7800
Dd		721	EVPQGQLGFYNAVAIPCCTTLTLQII.LPPEPLLKACRDNL.SQWEKYIRGETATWISSPSV	7860
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Dd		781	AOKAAASE 788	
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RESULT 8				
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DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE PDEL0A12.				
GN Name=Pdel0a;				
OS Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC Muridae; Murinae; Rattus.				
CX NCBI_TaxID=10116;				
OX NM	[1]			
RP NUCLEOTIDE SEQUENCE.				
RC STRAIN=M;				
RX PubMed=14752115; DOI=10.1074/jbc.M312500200;				
RA O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V.,				
RA De Zeeuw C.I., Singer G., Hunt S.P., Richter-Levin G., Mallet J.,				
RA Laroche S., Bliss T.V.P., French P.U.;				
RT "Differential amplification of intron-containing transcripts reveals				
RT long term potential-associated up-regulation of specific pdel0a				
RT phosphodiesterase splice variants.";				
RU J. Biol. Chem. 279.15841-15849(2004).				
DR EMBL, AY462092; AAC21244.1.-; mRNA.				
DR GO; GO:0004114; F:3,'5'-cyclic-nucleotide phosphodiesterase a. . ; IEA.				
DR GO; GO:0016787; F:hydrolyase activity; IEA.				
DR GO; GO:0007165; P:signal transduction; IEA.				
DR InterPro; IPR003607; Met_phos_hydro.				
DR InterPro; IPR002073; PDasease.				
DR Pfam; PF01590; GAF; 2.				



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OY 384 SRGSVIGVQWVNKISGSAFSGKTDENNFPMFAVFCALALHCANMYHRIHSECIYRYTME 443
DB 378 SRGSVIGVQWVNKISGSAFSGKTDENNFPMFAVFCALALHCANMYHRIHSECIYRYTME 437
OY 444 KLSYHSICTSEBMOGLMFMFLPARICRDIELFHPDIGPENNMPCI FYVMIHRSCTGSCF 503
DB 438 KLSYHSICTSEBMOGLMFMFLPARICRDIELFHPDIGPENNMPCI FYVMIHRSCTGSCF 497
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DB 498 ELEKLCRFIMSVKKNYRRVRYNNMKAATVVAHCAVAILQNNNGFLPTDERKGLLJACCH 557
OY 564 DLDRHGFNSNYLQKRDHPALALYSTSTMEQHHFSQTVSILQLEGNHIFSTLSSSEYEOVL 623
DB 558 DLDRHGFNSNYLQKRDHPALALYSTSTMEQHHFSQTVSILQLEGNHIFSTLSSSEYEOVL 617
OY 624 EIIRKAIITADLALYFGNKKOLEEMVQOTGSLNLHNSHSDRYVIGLMTACDLCSYTKLMP 683
DB 618 EIIRKAIITADLALYFGNKKOLEEMVQOTGSLNLHNSHSDRYVIGLMTACDLCSYTKLMP 677
OY 684 VTKLITANDIYAEFMAEGDEMKGIGIOPIMMDRDKRDEVPOGOLGFYNAVALPCYTTTLTQ 743
DB 678 VTKLITANDIYAEFMAEGDEMKGIGIOPIMMDRDKRDEVPOGOLGFYNAVALPCYTTTLTQ 737
OY 744 ILPTEPPLKACRDLNOMKEKVIIRGETAMWISGPGAPSKSTPEKLVNKYED 796
DB 738 ILPTEPPLKACRDLNOMKEKVIIRGETAMWIS--GPAISKSTSEKPRKXVD 788

RESULT 10
O6S9E9 RAT PRELIMINARY: PRT: 852 AA.
ID O6S9E9_1 RAT PRELIMINARY: PRT: 852 AA.
AC 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE PDB10A11.
CN Name=Pde10a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=M;
RX PubMed=14752115; DOI=10.1074/jbc.M31250200;
RA O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V.,
RA De Zeeuw C.I., Sanger G., Hunt S.P., Richter-Levin G., Mallet J.,
RA Laroche S., Blise T.V.P., French P.J.
RT "Differential amplification of intron-containing transcripts reveals
RT long term potentiation-associated up-regulation of specific Pde10A
RT phosphodiesterase splice variants."
RT J. Biol. Chem. 279:15841-15849(2004).
DR EMBL: AY462091; AAS21243.1; -; mRNA.
DR GO: GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0007165; F:signal transduction; IEA.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; Met_phos_hydro.
DR InterPro: IPR002073; PDase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDase_1; 1.
DR PRINTS: PR00387; PDIESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDASE_1; 1.
SQ SEQUENCE 852 AA, 95776 MW, 31FEB5D4DB8F60B CRC64;

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OY 84 VVYELANSYIEORLDTGGNNHLLYELSSIRIATYADDFALYFGECKNSLCVFPFPMK 143
DB 142 VVYELANSYIEORLDTGGNNHLLYELSSIRIATYADDFALYFGECKNSLCVFPFPMK 201
OY 144 EGQPLIPAGPIITQGTTSAYVAKSRTLVEDLIGDSRPPRGGLSEGTILQSVLCPI 203
DB 202 EGQPLIPAGPIITQGTTSAYVAKSRTLVEDLIGDSRPPRGGLSEGTILQSVLCPI 261
OY 204 VTALIGDLIGILEYRHMKEAFCLSHQEVATANTAMASVALIHQVCGSLAKQTELANFL 263
DB 262 VTALIGDLIGILEYRHMKEAFCLSHQEVATANTAMASVALIHQVCGSLAKQTELANFL 321
OY 264 LDVSKTYEDNIVALDLSLEHIMITYAKNLVADRCLAFVYDHKKNELYSDLPDISEKKGK 323
DB 322 LDVSKTYEDNIVALDLSLEHIMITYAKNLVADRCLAFVYDHKKNELYSDLPDISEKKGK 381
OY 324 PIFKTKKIRFSIEKGIAGVARGEVLTIPDAVADPRFNRVDTLTGTYTRNLICMFIY 383
DB 382 PIFKTKKIRFSIEKGIAGVARGEVLTIPDAVADPRFNRVDTLTGTYTRNLICMFIY 441
OY 384 SRGSVIGVQWVNKISGSAFSGKTDENNFPMFAVFCALALHCANMYHRIHSECIYRYTME 443
DB 442 SRGSVIGVQWVNKISGSAFSGKTDENNFPMFAVFCALALHCANMYHRIHSECIYRYTME 501
OY 444 KLSYHSICTSEBMOGLMFMFLPARICRDIELFHPDIGPENNMPCI FYVMIHRSCTGSCF 503
DB 442 KLSYHSICTSEBMOGLMFMFLPARICRDIELFHPDIGPENNMPCI FYVMIHRSCTGSCF 561
OY 504 ELEKLCRFIMSVKKNYRRVRYNNMKAATVVAHCAVAILQNNNGFLPTDERKGLLJACCH 563
DB 502 ELEKLCRFIMSVKKNYRRVRYNNMKAATVVAHCAVAILQNNNGFLPTDERKGLLJACCH 621
OY 564 DLDRHGFNSNYLQKRDHPALALYSTSTMEQHHFSQTVSILQLEGNHIFSTLSSSEYEOVL 623
DB 622 DLDRHGFNSNYLQKRDHPALALYSTSTMEQHHFSQTVSILQLEGNHIFSTLSSSEYEOVL 681
OY 624 EIIRKAIITADLALYFGNKKOLEEMVQOTGSLNLHNSHSDRYVIGLMTACDLCSYTKLMP 683
DB 682 EIIRKAIITADLALYFGNKKOLEEMVQOTGSLNLHNSHSDRYVIGLMTACDLCSYTKLMP 741
OY 684 VTKLITANDIYAEFMAEGDEMKGIGIOPIMMDRDKRDEVPOGOLGFYNAVALPCYTTTLTQ 743
DB 742 VTKLITANDIYAEFMAEGDEMKGIGIOPIMMDRDKRDEVPOGOLGFYNAVALPCYTTTLTQ 801
OY 744 ILPTEPPLKACRDLNOMKEKVIIRGETAMWISGPGAPSKSTPEKLVNKYED 796
DB 802 ILPTEPPLKACRDLNOMKEKVIIRGETAMWIS--GPAISKSTSEKPRKXVD 852

RESULT 11
PDE10 HUMAN STANDARD: PRT: 779 AA.
ID PDE10_HUMAN STANDARD: PRT: 779 AA.
AC 09Y233; 09Y571;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE CAMP and CAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A
DE (BC 3.1.4.17).
CN Name=PDE10A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM PDE10A1).
RC TISSUE=Fetal lung;
MEDLINE=99303608; PubMed=10373451; DOI=10.1074/jbc.274.26.18438;

```



RA Fujishige K., Kotera J., Michibata H., Yuasa K., Takebayashi S.-I.,  
 RA Okumura K., Omori K.;  
 RT "Cloning and characterization of a novel human phosphodiesterase that  
 RT hydrolyzes both cAMP and cGMP (PDE10A).";  
 RL J. Biol. Chem. 274:18438-18445(1999).  
 [2]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM PDE10A1), AND PARTIAL NUCLEOTIDE SEQUENCE  
 RP (ISOFORM PDE10A2).  
 RP TISSUE=Fetal brain;  
 RX MEDLINE=9921805; PubMed=10393245; DOI=10.1016/S0378-1119(99)00171-7;  
 RA Loughney K., Snyder P.B., Uher L., Rosman G.J., Ferguson K.,  
 RA Florio V.A.;  
 RT "Isolation and characterization of PDE10A, a novel human 3',5'-cyclic  
 RT nucleotide phosphodiesterase.";  
 RL Gene 234:109-117(1999).  
 CC -1- FUNCTION: Plays a role in signal transduction by regulating the  
 CC intracellular concentration of cyclic nucleotides. This enzyme can  
 CC hydrolyze both cAMP and cGMP, having a higher affinity for cAMP.  
 CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =  
 CC nucleoside 5'-phosphate.  
 CC -1- COFACTOR: Divalent cations.  
 CC -1- ENZYME REGULATION: Inhibited by dipyrindamole and moderately by  
 CC IBMX. cAMP potentially inhibits hydrolysis of cGMP.  
 CC -1- SUBCELLULAR LOCATION: Located mostly to soluble cellular  
 CC fractions.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Isoforms differ in their N-terminal region;  
 CC Name=PDE10A1; Sequence=Displayed;  
 CC IsoId=Q91233-1; Sequence=VSP\_004601;  
 CC Name=PDE10A2;  
 CC IsoId=Q91233-2; Sequence=VSP\_004601;  
 CC Note=Incomplete sequence;  
 CC -1- TISSUE SPECIFICITY: Abundant in the putamen and caudate nucleus  
 CC regions of brain and testis, moderately expressed in the thyroid  
 CC gland, pituitary gland, thalamus and cerebellum.  
 CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two  
 CC putative divalent metal sites and an N-terminal regulatory domain  
 CC which contains one putative cGMP-binding region.  
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
 CC family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AB020593; BAA78034.1; -; mRNA.  
 CC EMBL; AF127479; AAD32595.1; -; mRNA.  
 CC EMBL; AF127480; AAD32596.1; -; mRNA.  
 CC PDB; 1LRB; Model; A=501-757.  
 CC Ensembl; ENSG00000112541; Homo sapiens.  
 CC HGNC; HGNC:8772; PDE10A.  
 CC GO; GO:0004114; F.3.3',5'-cyclic-nucleotide phosphodiesterase a. . .; TAS.  
 CC InterPro; IPR003018; GAF.  
 CC InterPro; IPR002073; PDBase.  
 CC Pfam; PF00233; PDBase; 1, 1.  
 CC PRINTS; PR00387; PD1ESTERSB1.  
 CC PROSITE; PS00126; PDBASE; 1, 1.  
 CC 3D-structure; Alternative splicing; cGMP; cGMP-binding; Hydrolyase;  
 CC Nucleotide-binding; Polymorphism.  
 CC NP BIND 339 416 cGMP (By similarity).  
 CC BINDING 386 386 cGMP (By similarity).  
 CC BINDING 387 387 cGMP (By similarity).  
 CC BINDING 397 397 cGMP (By similarity).  
 CC VARSPLIC 1 13 NR1E8RSQHLTG -> QGASFLAANAALLFGSDMEDGPS  
 CC NNA5CFRLTECFASPS (in isoform PDE10A2).  
 CC /FTId=VSP\_004601.  
 CC L->P.  
 CC /FTId=VAR\_008797  
 CC VARIANT 303 303  
 CC SEQUENCE 779 AA; 88412 MW; C561BBB524A32B7 CRC64;

Query Match 92.2%; Score 3878; DB 1; Length 779;  
 Best Local Similarity 95.4%; Pred. No. 5.2e-291;  
 Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;  
 24 LTDEKVKAYLSLHPVDLDFVSESVSAETVEKMLRKTKNAKDDESPKVSRYQDTNNQ 83  
 14 LTDEKVKAYLSLHPVDLDFVSESVSAETVEKMLRKTKNAKDDESPKVSRYQDTNNQ 73  
 84 VVEELNSYIEORLDGTGGNNHLLYLSSTIRATATADGALYFLGECNNSLCVFIPGK 143  
 74 VVEELNSYIEORLDGTGGNNHLLYLSSTIRATATADGALYFLGECNNSLCVFIPGK 133  
 144 EGQPLIAGPTTQSTTSAYAVAKSKTLYVDLIDGDEFPFGTGESGTRIQSVLCPI 203  
 134 EGQPLIAGPTTQSTTSAYAVAKSKTLYVDLIDGDEFPFGTGESGTRIQSVLCPI 193  
 204 VTAIGDLIGILELYHMGKEAFCLSHQEVATNLMASVAILHVOVCRLAKQTEINDEL 263  
 194 VTAIGDLIGILELYHMGKEAFCLSHQEVATNLMASVAILHVOVCRLAKQTEINDEL 253  
 264 LDVSKTYEDNIVAILDLEHITVAKNLYNADRCALFOVDHKKSLYSDFPIGEEKK 323  
 254 LDVSKTYEDNIVAILDLEHITVAKNLYNADRCALFOVDHKKSLYSDFPIGEEKK 313  
 324 PTFKTKTERFSIEKGIAGVARTGEVNI PDAYADPRRERVDLYTGYTTRNIIICMP 383  
 314 PTFKTKTERFSIEKGIAGVARTGEVNI PDAYADPRRERVDLYTGYTTRNIIICMP 373  
 384 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAVMYRIRHSBICRYTNE 443  
 374 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAVMYRIRHSBICRYTNE 433  
 444 KLSYHSICTSEEMOGLMRENLPAICRDIELFHPDIGPEENMPGIFVTMIRSCISCF 503  
 434 KLSYHSICTSEEMOGLMRENLPAICRDIELFHPDIGPEENMPGIFVTMIRSCISCF 493  
 504 ELEKLCRFIMSYKQYRRRPYNNWGAATVAVACMAIILONNGLFTDLRRKGLIACLG 563  
 494 ELEKLCRFIMSYKQYRRRPYNNWGAATVAVACMAIILONNGLFTDLRRKGLIACLG 553  
 564 DLDRGFNSYLOKFPDPLAALYSTTMEQHPSQVSLIQLEGNHIFSTLSSEBEQVL 623  
 554 DLDRGFNSYLOKFPDPLAALYSTTMEQHPSQVSLIQLEGNHIFSTLSSEBEQVL 613  
 624 EIIIRKAIITDIALYFGNKKOLEBMYQTGSLNLHNSHEDRYIGLMTACDLCSTVKLP 683  
 614 EIIIRKAIITDIALYFGNKKOLEBMYQTGSLNLHNSHEDRYIGLMTACDLCSTVKLP 673  
 684 VTKLTANDIYAEFMAAGDEMKKLGIOPIPMMDRDKDDEVPQGLGYNAVALPCYTTLTQ 743  
 674 VTKLTANDIYAEFMAAGDEMKKLGIOPIPMMDRDKDDEVPQGLGYNAVALPCYTTLTQ 733  
 744 ILPTEPLILACRDNLNOMEKVI RGETAMWISGPPAPSKSTPE 788  
 734 ILPTEPLILACRDNLNOMEKVI RGETAMWISGPPAPSKSTPE 778  
 RESULT 12  
 Q9NTV4\_HUMAN PRELIMINARY; PRT; 779 AA.  
 ID Q9NTV4\_HUMAN PRELIMINARY; PRT; 779 AA.  
 AC Q9NTV4\_HUMAN PRELIMINARY; PRT; 779 AA.  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Phosphodiesterase 10A.  
 GN Name=PDE10A; ORFNames=RP3-416F21.1-001;  
 OS Homo sapiens (human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]

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RA NUCLEOTIDE SEQUENCE.
RA Martin S.; (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN Submitted
[2]
RN NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RV [3]
RV NUCLEOTIDE SEQUENCE.
RA Laird G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL117345; CAB92797.2; -; Genomic DNA.
DR EMBL; AL136130; CAI20436.1; -; Genomic DNA.
DR EMBL; AL160160; CAH72023.1; -; Genomic DNA.
DR EMBL; AL160160; CAB92797.2; JOINED; Genomic DNA.
DR EMBL; AL160160; CAB92797.2; JOINED; Genomic DNA.
DR EMBL; AL117345; CAH72023.1; JOINED; Genomic DNA.
DR EMBL; AL160160; CAI20436.1; JOINED; Genomic DNA.
DR EMBL; AL117345; CAH72023.1; JOINED; Genomic DNA.
DR EMBL; AL136130; CAH72023.1; JOINED; Genomic DNA.
DR EMBL; ENSG00000112541; Homo sapiens.
DR GO; GO:0004114; P:3, '5'-cyclic-nucleotide phosphodiesterase a. . ; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003019; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDasee.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDasee_I; 1.
DR PRINTS; PRO0387; PDSESTERASE1.
DR SMART; SMO0055; GAF; 2.
DR SMART; SMO0471; Hdc; 1.
DR PROSITE; PS00126; PDasee_I; 1.
DR SEQUENCE 779 AA; 88412 MW; C5651BBB524A32B7 CRC64;
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Query Match	92.2%	Score 3878	DB 2	Length 779
Best Local Similarity	95.4%	Pred. No. 5.2e-291		
Matches 730	Conservative 19	Mismatches 16	Indels 0	Gaps 0
Qy	LTDEKVKAYLSLHPVLDFEVSSESAETVEKMLKRTKAKXDEPSKVSRYODTNMGG		14	1
Db	LITDEKVKAYLSLHPVLDFEVSSESAETVEKMLKRNKKNSXDESAFKVSRYSQDTNMGG		14	1
Qy	VYVEINASTIEORLDTGCGDNHLLLYELSSITIRATKADGALYFLGECNNSLCYFIPPGK		84	143
Db	VYVEINASTIEORLDTGCGDNQLLLYELSSITIKIATKADGALYFLGECNNSLCIPPGK		74	133
Qy	EGOPRLIAGPFTTGGTTISAVYAKSRKTLVNDIGDEPFGTGLSGSTRISQVLCPI		144	203
Db	EGKPLIAGPFTTGGTTISAVYAKSRKTLVEDILGDEPFGTGLSGSTRISQVLCPI		134	193
Qy	VTAIGDLIGILELYRHWGKEAFLSHOEVAVTANLAWASVAIHQVYCRGLAKOTELNDFL		204	263
Db	VTAIGDLIGILELYRHWGKEAFLSHOEVAVTANLAWASVAIHQVYCRGLAKOTELNDFL		194	253
Qy	LDVSKTYPDNVAISLSLEHMITAKNLVNAARCLFQVDHKKELYSOLFIDGEKEX		264	323
Db	LDVSKTYPDNVAISLSLEHMITAKNLVNAARCLFQVDHKKELYSOLFIDGEKEX		254	313
Qy	PIFKTKELRFSIEKGIAGQVARTGEVLNI PDVADPRFNREVDLYGTGTTNII LCMPIV		324	383
Db	PVFKTKELRFSIEKGIAGQVARTGEVLNI PDVADPRFNREVDLYGTGTTNII LCMPIV		314	373
Qy	SRGSVIGAVQWVKISGSAFSTKDENEPMFAVFCALALHCANMYRIRHSECTIYVYME		384	443
Db	SRGSVIGAVQWVKISGSAFSTKDENEPMFAVFCALALHCANMYRIRHSECTIYVYME		374	433
Qy	KLSTYSICTSEEMOGLMRFNLPAICRDLLEHPDIPGPNMPCGFVYMIRHSCGTCGF		444	503
Db	KLSTYSICTSEEMOGLMRFNLPAICRDLLEHPDIPGPNMPCGFVYMIRHSCGTCGF		434	493
Qy	ELEKLCRFIMSYKKNYRRVYHNMKGLAVVAHGMVALIDNNNGLPFLTERKGLIACLCH		504	563

Db	494	ELBKCGRFMSVKQNYRRPVRPNYMHGAVTVAHSMYALIQNNHTLTFTDERKGLLIACLCH	553
Qy	564	DLDRHGFSSNYIQKEDHPALALYSTSTMEQNNHPSQYTSIIQLEBHNIFSTLSSSEYQVL	623
Db	554	DLDRHGFSSNYIQKEDHPALALYSTSTMEQNNHPSQYTSIIQLEBHNIFSTLSSSEYQVL	613
Qy	624	EIIRKAIITDIALYFGNRCOLEBNYQGTSLNLIHQSHDRDIVGLMPTACDLCSTYGLMP	683
Db	614	EIIRKAIITDIALYFGNRCOLEBNYQGTSLNLIHQSHDRDIVGLMPTACDLCSTYGLMP	673
Qy	684	VTQLTANDIYAEFWAEGDEMKKLGIOPIPMMDRDRCDEVPOGLGFYNAVALPCYTLTLQ	743
Db	674	VTQLTANDIYAEFWAEGDEMKKLGIOPIPMMDRDRCDEVPOGLGFYNAVALPCYTLTLQ	733
Qy	744	ILPPTPEPLKACRDNIHQEKYIRREBEETAMTISGCGRAPSKSTTE	788
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DT	05-JUL-2004 (TREMblrel_27, Created)
DT	05-JUL-2004 (TREMblrel_27, Last sequence update)
DT	05-JUL-2004 (TREMblrel_27, Last annotation update)
DE	PDE10A protein.
GN	Name=PDE10A;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheta; Euarchontoglires; Primates; Catarrhini; Homnidae;
CC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Halleck A., Ebert L., M'koundinya M., Schick M., Sisenstein S.,
RA	Newbert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA	Korn B., Zhuo D., Hu Y., Labber J.;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; CR536567; CAG38804.1; -. mRNA.
DR	GO; GO:0004114; F:3,5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.
DR	GO; GO:0016787; P:hydrolase activity; IEA.
DR	GO; GO:007165; P:signal transduction; IEA.
DR	InterPro; IPR03018; GAF.
DR	InterPro; IPR003607; Met_phos_hydro.
DR	InterPro; IPR02073; PDBase.
DR	pfam; PF01590; GAF_2.
DR	pfam; PF00233; PDBase_I_1.
DR	PRINTS; PR00387; PDIESTERASE1.
DR	SMART; SM0065; GAF_2.
DR	SMART; SM00471; Hdc_1.
DR	PROSITE; PS00126; PDbase_I_1.
SQ	SEQUENCE 779 AA; 88442 MW; DA5A127B464A32B7 CRC64;
Query Match 92.1%; Score 3872; DB 2; Length 779;	
Best local similarity 95.3%; Pred. No. 1,56-250;	
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;	
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DB	14 LTDERKVAAYVLSIHPOVLDFPVSSVSATVEVKMLKRKNNSSEDSAPKEVSRYODTNNG 73
OY	VVEELNSYIEORLTGTGGDNHLLVELSIIIRIATKADGALYFFGECSNLSCLVFIPGMK 143
DB	74 VVEELNSYIEORLTGTGGDNQLLVLESIITIKATKGAFALYFFGECSNLSCLFTPPRIK 133
OY	EGGRLLIPAGEITIGTTISAVVAASKRTLVEDIILGDREFRFGTGLSGTRIQSVLCPI 203
DB	EGGRRLIPAGITIGTTTSASVAVSKRTLVEDIILGDERFRFGTGLSGTRIQSVLCPI 193
OY	VTAIAGDLIGILELRHNHGKAFCLSHOBVATANIAMASVAIHQOVCGRLAKQTBLNDFL 263
DB	VTAIAGDLIGILELRHNHGKAFCLSHOBVATANIAMASVALHQOVCGRLAKQTBLNDFL 253

QY 264 LDVSKTYFDNIIVADISLLEHIMITYAKNLVNAADRCALFOVDHONKELYSDFDIGEEKK 323  
 DB 264 LDVSKTYFDNIIVADISLLEHIMITYAKNLVNAADRCALFOVDHONKELYSDFDIGEEKK 313  
 QY 324 PIFKTKTEIRFSEIEKGIAGQVARTGEVLNIPDAVADPRRREVDLYTGTTRNIIICMPIV 383  
 DB 324 PIFKTKTEIRFSEIEKGIAGQVARTGEVLNIPDAVADPRRREVDLYTGTTRNIIICMPIV 373  
 QY 384 SMGSYIGVQVQWVKISGSAFSTKDENNFQPAVFCALALHCANMYHRIHSECIYATME 443  
 DB 384 SMGSYIGVQVQWVKISGSAFSTKDENNFQPAVFCALALHCANMYHRIHSECIYATME 433  
 QY 444 KLSYHSICTSEBMOGLMRPNLPARICRDIELFPHDIGPEENMPGIFVYMIHSCGTCSE 503  
 DB 444 KLSYHSICTSEBMOGLMRPNLPARICRDIELFPHDIGPEENMPGIFVYMIHSCGTCSE 493  
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 DB 504 ELBKLCRFPTMSYKQNRVRYPIYHNMKHAIVVAHCMYAILLONNGLFTDLERKGLIACLC 553  
 QY 564 DLDHGFSSSYLOKPHPLAALYSTSTMEQHPSQTVSILQLEGHNIFFSTLSSEYEQYL 623  
 DB 564 DLDHGFSSSYLOKPHPLAALYSTSTMEQHPSQTVSILQLEGHNIFFSTLSSEYEQYL 613  
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 DB 624 EIRKKAIIATDIALYFNGRKOLEEMVQTSGLNLHNSHRDVIGLMWTACDLCSTVKMP 673  
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 DB 684 VTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRKDEVPQGLGFYNAVAIPCYTTLLQ 733  
 QY 744 IIPPEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPE 786  
 DB 744 IIPPEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPE 776  
 QY 734 IIPPEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPE 778  
 DB 734 IIPPEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPE 778  
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 AC Q6S9E7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE PDB10A13.  
 GN Name=Pdel10a;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 RX NCBI\_Taxid=10116;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=M;  
 RC PubMed=14752115; DOI=10.1074/jbc.M312500200;  
 RA O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V.,  
 RA De Zeeuw C.I., Sanger G., Hunt S.P., Richerter-Levin G., Mallet J.,  
 RA Laroche S., Blais T.V.P., French P.J.;  
 RT "Differential amplification of intron-containing transcripts reveals  
 RT long term potential-associated up-regulation of specific Pdel10A  
 RT phosphodiesterase splice variants."  
 RT J. Biol. Chem. 279.15841-15849(2004).  
 RL EMBL; AY62093; AA621245.1; mRNA.  
 DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR003018; GAF.  
 DR InterPro; IPR003607; Met\_pho\_hydro.  
 DR InterPro; IPR002073; pDasee.  
 DR Pfam; PF01590; GAF; 2.  
 DR Pfam; PF00233; pDasee; 1.  
 DR PRINTS; PRO0387; PDIESTERASE1.

DR SMART; SM00065; GAF; 2.  
 DR SMART; SM00471; HDC; 1.  
 DR PROSITE; PS00126; PDASE\_1; 1.  
 DR SEQUENCE 714 AA; 81028 MW; 5ABCD3669558F6 CRC64;  
 SQ  
 Query Match 88.3%; Score 3715; DB 2; Length 714;  
 Best Local Similarity 98.5%; Pred. No. 1.9e-278;  
 Matches 705; Conservative 2; Mismatches 7; Indels 2; Gaps 1;  
 QY 81 MGVVYELNSYEQRLDTGGDNHLLLYELSSIRATADGALYFLGCONSLCVFIP 140  
 DB 1 MGVVYELNSYEQRLDTGGDNHLLLYELSSIRATADGALYFLGCONSLCVFIP 60  
 QY 141 GMEGQPLIPAGPIITOGTTISAVYAKSRKTLVVDIIGDEFPFGTGLSESTRIQSVLC 200  
 DB 61 GMEGQPLIPAGPIITOGTTISAVYAKSRKTLVVDIIGDEFPFGTGLSESTRIQSVLC 120  
 QY 201 LPITVAIGDLIGILEYRHMGEKAFCLSHQEVATNLAWASVAIHQVYCRGLAQTEIN 260  
 DB 121 LPITVAIGDLIGILEYRHMGEKAFCLSHQEVATNLAWASVAIHQVYCRGLAQTEIN 180  
 QY 261 DFLDVSKTYFDNIIVADISLLEHIMITYAKNLVNAADRCALFOVDHONKELYSDFDIGEEK 320  
 DB 181 DFLDVSKTYFDNIIVADISLLEHIMITYAKNLVNAADRCALFOVDHONKELYSDFDIGEEK 240  
 QY 321 EKKPIFKTKTEIRFSEIEKGIAGQVARTGEVLNIPDAVADPRRREVDLYTGTTRNIIICM 380  
 DB 241 EKKPIFKTKTEIRFSEIEKGIAGQVARTGEVLNIPDAVADPRRREVDLYTGTTRNIIICM 300  
 QY 381 PIVSGSVIGVQVQWVKISGSAFSTKDENNFQPAVFCALALHCANMYHRIHSECIYAV 440  
 DB 301 PIVSGSVIGVQVQWVKISGSAFSTKDENNFQPAVFCALALHCANMYHRIHSECIYAV 360  
 QY 441 TMEKLSYHSICTSEBMOGLMRPNLPARICRDIELFPHDIGPEENMPGIFVYMIHSCGTCSE 500  
 DB 361 TMEKLSYHSICTSEBMOGLMRPNLPARICRDIELFPHDIGPEENMPGIFVYMIHSCGTCSE 420  
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 DB 421 SCEPELKC RFPTMSYKQNRVRYPIYHNMKHAIVVAHCMYAILLONNGLFTDLERKGLIAC 480  
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 QY 621 QVLEIRKKAIIATDIALYFNGRKOLEEMVQTSGLNLHNSHRDVIGLMWTACDLCSTVK 680  
 DB 541 QVLEIRKKAIIATDIALYFNGRKOLEEMVQTSGLNLHNSHRDVIGLMWTACDLCSTVK 600  
 QY 681 LMPVTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRKDEVPQGLGFYNAVAIPCYTT 740  
 DB 601 LMPVTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRKDEVPQGLGFYNAVAIPCYTT 660  
 QY 741 LTPILPTEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPEKLVAYED 796  
 DB 661 LTPILPTEPLKACQDNINOMKXVIRGETAMWISGPAPEKSTPEKLVAYED 714  
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 AC Q9HCP9;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE PDB10A13 (EC 3.1.4.17) (Fragment).  
 GN Name=HSPD10A;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_Taxid=9606;  
 RN NCBI\_Taxid=9606;  
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RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20453115; PubMed=10998054;  
RA Fujishige K., Kotera J., Yuasa K., Omori K.;  
RT "The human phosphodiesterase PDE10A gene. Genomic organization and  
evolutionary relatedness with other PDEs containing GAF domains.";  
RL Eur. J. Biochem. 267:5943-5951(2000).  
DR EMBL; AB041798; BAB16383.1; -; Genomic DNA.  
DR GO; GO:0004114; P.3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.  
DR GO; GO:0016787; P:hydrolyase activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDBase.  
DR Pfam; PF00233; PDBase\_1; 1.  
DR PRINTS; PR00387; PD1ESTERASE1.  
DR SMART; SM00065; GAF; 2.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDBASE\_1; 1.  
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FT NON\_TER 1 1  
SQ SEQUENCE 714 AA; 80887 MW; 0C43F60A307CCDF0 CRC64;  
  
Query Match 86.5%; Score 3639; DB 2; Length 714;  
Best Local Similarity 95.8%; Pred. No. 1.5e-272;  
Matches 683; Conservative 16; Mismatches 14; Indels 0; Gaps 0;  
  
QY 76 YODTMQGVVYELNSYIEQRLDPTGGDNHLLLYELSSIIRIATKADGFALYFLGECNNSLC 135  
DB 1 YODTMQGVVYELNSYIEQRDLDTGGDNQLLYELSSIIKIATKADGFALYFLGECNNSLC 60  
QY 136 VEIPGMEKGOPRLIPAGPIITOGTTISAVVAKSRKTLVLEDILGDERPFRGTGLSGTRI 195  
DB 61 ITPPGIIEGKPRLLIPAGPIITGTTISAVVAKSRKTLVLEDILGDERPFRGTGLSGTRI 120  
QY 196 QSVLCPLVTATGDLIGILELYRHNGKEAFCLSHOEVAATANLAMASVAITHQVQVCRGLAK 255  
DB 121 QSVLCPLVTATGDLIGILELYRHNGKEAFCLSHOEVAATANLAMASVAITHQVQVCRGLAK 180  
QY 256 QTELNDPLLDVSKTYFDNIVAIDSLLEHIMYAKLVNADRCALFQVDHKNKELYSDFD 315  
DB 181 QTELNDPLLDVSKTYFDNIVAIDSLLEHIMYAKLVNADRCALFQVDHKNKELYSDFD 240  
QY 316 IGEERKGPPIPKKTEIRPSIEKGIAGVARTGEVLTIPDAVADPRENREVDLYGTTR 375  
DB 241 IGEERKGPVFPKTEIRPSIEKGIAGVARTGEVLTIPDAVADPRENREVDLYGTTR 300  
QY 376 NILCMPIVSRGSGVIGVQVQVNIISGSAFSTDENNFQMFVFCALALHCANNYHRIHSE 435  
DB 301 NILCMPIVSRGSGVIGVQVQVNIISGSAFSTDENNFQMFVFCALALHCANNYHRIHSE 360  
QY 436 CIYRVTMKLSYHSICTSEEWQGLKRFNIPARICRDIELFHFIDIGPENMPGIFVYMIH 495  
DB 361 CIYRVTMKLSYHSICTSEEWQGLKRFNIPARICRDIELFHFIDIGPENMPGIFVYMIH 420  
QY 496 RSCGTSCELEKLCRFINSVKKNYRVPYHNKHAHTVAHCMTALLQNNHTLFTDLERKG 555  
DB 421 RSCGTSCELEKLCRFINSVKKNYRVPYHNKHAHTVAHCMTALLQNNHTLFTDLERKG 480  
QY 556 LLIACTCHDLDRGFSNSYLOKFDHPLAALYSTSTMEQHFSQTVSIIQLEGHNIFFSTLS 615  
DB 481 LLIACTCHDLDRGFSNSYLOKFDHPLAALYSTSTMEQHFSQTVSIIQLEGHNIFFSTLS 540  
QY 616 SSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSINLNQSHDRVIGIMMTACDL 675  
DB 541 SSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSINLNQSHDRVIGIMMTACDL 600  
QY 676 CSVTGLMPPTKLTANDIYAEFAEGDEMKGIGIPIPMMDRDKRDEVPGQGLGFYNAVAI 735  
DB 601 CSVTGLMPPTKLTANDIYAEFAEGDEMKGIGIPIPMMDRDKRDEVPGQGLGFYNAVAI 660  
QY 736 PCYTLTQILPPTBPLKACRDNLQMEKVIIRGEETAMWISGPGPAPSKSTPE 788  
DB 661 PCYTLTQILPPTBPLKACRDNLQMEKVIIRGEETAMWISGPGPAPSKSTPE 713

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Search completed: January 10, 2006, 13:55:30  
Job time : 83 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 10, 2006, 13:52:10 ; Search time 27 Seconds  
(without alignments)  
2437.401 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206

Sequence: 1 MEDGSPNNASCFRRLTBCFL.....GGPAPSKSTPEKLVNVED 796

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*

2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3997	95.0	803	1 US-08-951-648-4	Sequence 4, Appl
2	3997	95.0	803	2 US-09-174-437-4	Sequence 4, Appl
3	3997	95.0	803	2 US-09-686-055A-4	Sequence 4, Appl
4	3878	92.2	779	1 US-08-951-648-6	Sequence 6, Appl
5	3878	92.2	779	2 US-09-174-437-6	Sequence 6, Appl
6	3878	92.2	779	2 US-09-686-055A-6	Sequence 6, Appl
7	3878	92.2	779	2 US-09-420-190-1	Sequence 1, Appl
8	3873	92.1	766	1 US-08-951-648-2	Sequence 2, Appl
9	3873	92.1	766	2 US-09-174-437-2	Sequence 2, Appl
10	3873	92.1	766	2 US-09-686-055A-2	Sequence 2, Appl
11	1010	24.0	1284	2 US-10-296-144-5	Sequence 5, Appl
12	918	21.8	875	1 US-08-480-547A-10	Sequence 10, Appl
13	918	21.8	875	1 US-08-250-847B-10	Sequence 10, Appl
14	918	21.8	875	1 US-08-463-949A-10	Sequence 10, Appl
15	918	21.8	875	2 US-08-464-410A-10	Sequence 10, Appl
16	914	21.7	875	4 PCT-US94-06066-10	Sequence 10, Appl
17	912.5	21.7	875	1 US-08-480-547A-23	Sequence 23, Appl
18	912.5	21.7	875	1 US-08-250-847B-23	Sequence 23, Appl
19	912.5	21.7	875	1 US-08-463-949A-23	Sequence 23, Appl
20	912.5	21.7	875	1 US-08-464-410A-23	Sequence 23, Appl
21	912.5	21.7	875	2 US-09-226-741-5	Sequence 5, Appl
22	912.5	21.7	875	2 US-09-595-514-5	Sequence 5, Appl
23	912.5	21.7	875	2 US-09-949-002-310	Sequence 310, Appl
24	912.5	21.7	875	4 PCT-US94-06066-23	Sequence 23, Appl
25	909	21.6	921	1 US-07-872-644-39	Sequence 39, Appl
26	909	21.6	921	1 US-08-297-494-39	Sequence 39, Appl
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ALIGNMENTS

28	909	21.6	921	1 US-08-479-532-39	Sequence 39, Appl
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30	909	21.6	921	1 US-08-455-526-39	Sequence 39, Appl
31	909	21.6	921	2 US-09-139-491-39	Sequence 39, Appl
32	909	21.6	921	2 US-09-754-250-5	Sequence 5, Appl
33	909	21.6	921	2 US-09-883-825-39	Sequence 39, Appl
34	909	21.6	921	2 US-10-094-989-5	Sequence 5, Appl
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36	908	21.6	942	1 US-07-872-644-43	Sequence 43, Appl
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39	908	21.6	942	1 US-08-479-532-43	Sequence 43, Appl
40	908	21.6	942	1 US-08-455-526-43	Sequence 43, Appl
41	908	21.6	942	1 US-08-455-526-43	Sequence 43, Appl
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43	908	21.6	942	2 US-09-883-825-43	Sequence 43, Appl
44	908	21.6	942	4 PCT-US92-03222-43	Sequence 43, Appl
45	897.5	21.3	920	2 US-09-754-250-2	Sequence 2, Appl

RESULT 1  
US-08-951-648-4  
Sequence 4, Application US/08951648  
Patent No. 5932465  
GENERAL INFORMATION:  
APPLICANT: Loughney, Kate  
TITLE OF INVENTION: Phosphodiesterase 8  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum  
STREET: 233 South Wacker, Sears Tower Suite 6300  
CITY: Chicago  
STATE: Illinois  
COUNTRY: US  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/951,648  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27866/34038  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 803 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-951-648-4  
Query Match 95.0%; Score 3997; DB 1; Length 803;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRLTBCFLPSLTDEKVKAYISLHPVLDERVSVSAETVEKYLK 60  
DB 15 MEDGSPNNASCFRRLTBCFLPSLTDEKVKAYISLHPVLDERVSVSAETVEKYLK 74  
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DB 75 NKSEBSAPKESRYQDTNMGGVYELNSYIEQRIDTGGDNHLLLYELSSIRIATKAD 134

Oy	121	GPALYPLGBCNNSLCVPIPRGKKEQOPRLIPAGPITQCTTISANVAKSKRTLLVBEILD	180
Db	135	GFALYFLGBCNNSLCTFTPPGKKEGPRLIPAGPITQCTTISANVAKSKRTLLVBEILD	194
Oy	181	BRFPKGTGSESTRIOSVLCPIVTAIGDLIGLIELYRHMGEAFLCSHQEVATANLAMA	240
Db	195	BRFPKGTGSESTRIOSVLCPIVTAIGDLIGLIELYRHMGEAFLCSHQEVATANLAMA	254
Oy	241	SVAIHQOVQCRGLAQTELENDFLDVSKTYFNNIYAIDSLIHMIMYAOLVNAIDRCALF	300
Db	255	SVAIHQOVQCRGLAQTELENDFLDVSKTYFNNIYAIDSLIHMIMYAOLVNAIDRCALF	314
Oy	301	QVDHNGKELYSDFPIGEEKGKPIFKTKKEIRFSIEKJAGQVARTGEVLNI PDAVADP	360
Db	315	QVDHNGKELYSDFPIGEEKGKPPFKTKKEIRFSIEKJIAQVARTGEVLNI PDAVADP	374
Oy	361	RPNREVDLYGTGTNNILCMPIVSRGSVIGVQVONKISGSAPSKTDENNPFQFAVCAL	420
Db	375	RPNREVDLYGTGTNNILCMPIVSRGSVIGVQVONKISGSAPSKTDENNPFQFAVCAL	434
Oy	421	ALHGANMTHRIHSHSCIRYVTEKLSYHSICTSEBQGLARFNLPARICRDIELPFHDG	480
Db	435	ALHGANMTHRIHSHSCIRYVTEKLSYHSICTSEBQGLAQFTLPRLCKEILEHFDIG	494
Oy	481	PFENNMPGIFVYMIHRSCTGSCFELEKLCRFITMSYKKNRAVYPYHNKKAVTVAHCMAI	540
Db	495	PFENNMPGIFVYMWARSCTGSCFELEKLCRFITMSYKKNRAVYPYHNKKAVTVAHCMAI	554
Oy	541	LONNNGLTDLERKILITACICHDIDHGFNSYLOKPHPLAALYSTSTMOHHSQV	600
Db	555	LONNHTLTDLERKILITACICHDIDHGFNSYLOKPHPLAALYSTSTMOHHSQV	614
Oy	601	SILQEGHNIFSTLSSSEYEQVLEIIRKAI IATDIALYFGNRKQLEMYQTSILNINOS	660
Db	615	SILQEGHNIFSTLSSSEYEQVLEIIRKAI IATDIALYFGNRKQLEMYQTSILNINOS	674
Oy	661	HRDRYIGLMTACDLCSTYKLMPTVKLTANDIYAEFWAAGDEMKKLGIOPIPMNDRKXD	720
Db	675	HRDRYIGLMTACDLCSTYKLMPTVKLTANDIYAEFWAAGDEMKKLGIOPIPMNDRKXD	734
Oy	721	EVPQGLGFYNAVAIPCYTTLTQILPPTPEPLAKACRDNIINQMEKYIRGETAMWISGPGP	780
Db	735	EVPQGLGFYNAVAIPCYTTLTQILPPTPEPLAKACRDNIINQMEKYIRGETAMWISPSV	794
Oy	781	APSKSTPE 788	
Db	795	AOKAAASE 802	
RESULT 2			
US-09-174-437-4			
; Sequence 4, Application US/09174437A			
; Patent No. 6133007			
; GENERAL INFORMATION:			
; APPLICANT: Loughney, Kate			
; TITLE OF INVENTION: Phosphodiesterase 8A			
; FILE REFERENCE: 27866/35047			
; CURRENT APPLICATION NUMBER: US/09/174,437A			
; CURRENT FILING DATE: 1998-10-16			
; EARLIER APPLICATION NUMBER: 08/951,648			
; EARLIER FILING DATE: 1997-10-16			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 4			
; LENGTH: 803			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; US-09-174-437-4			

	Score	DB 2	Length	803
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Best Local Similarly	95.4%	Pred. No. 0		
Matches 752; Conservative	19	Mismatches	0	Gaps 0

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QY	61	TNKADEBS	PREVSHYODTNMGVVYEINSYIEQRLDITGGDHMLLYELSSIIIRATKAD	120
Db	75	NKSGDEBA	PREVSHYODTNMGVVYEINSYIEQLDLTGGDQMLLYELSSIIIRATKAD	134
QY	121	GPALYFLCE	CNNLSLCVFIPRGMKEGQPRLLIPAGPTTTCGTTTATYAKSKTLLVEBILCD	180
Db	135	GFALYFLCE	CNNLSLCIFTPRPGIKKQPRLLIPAGPTTTCGTTTASAYAKSKTLLVEBILCD	194
QY	181	ERFPFGTLE	SGSTRQSQVLCPIYVAIGDLIGILEYRHMGKEAFCLSHQEVATANILAMA	240
Db	195	ERFPFGTLE	SGSTRQSQVLCPIYVAIGDLIGILEYRHMGKEACLSHQEVATANILAMA	254
QY	241	SVAIHQVOC	BGLAKOTELNDFLDVSKTYFDNIYVAIDSLHEHIMYAKNLVNADECALF	300
Db	255	SVAIHQVOC	BGLAKOTELNDFLDVSKTYFDNIYVAIDSLHEHIMYAKNLVNADECALF	314
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Db	315	QVDHKNKEL	YSDLPDPIGEKXEGKPRFKTKKEIRSEIEKGIAGQVARTGVNLIPDAYADP	374
QY	361	RPNREVDLY	TGTYTRNIIICMPIVSRGSYIVGVQWANKISGSAFSKTDENPFQMAFVICAL	420
Db	375	RPNREVDLY	TGTYTRNIIICMPIVSRGSYIVGVQWANKISGSAFSKTDENPFQMAFVICAL	434
QY	421	ALHCANMYH	IRHSECIYRVTMKEKLSYHSICTSEBWOGLMREPNLPAICRODTIELFHEIDIG	480
Db	435	ALHCANMYH	IRHSECIYRVTMKEKLSYHSICTSEBWOGLMREPNLPAICRODTIELFHEIDIG	494
QY	481	PFEANMPCII	PFYMMIHRSGCTSCFELEKICRFPMYSKXNYRVRPYNNMKXAVVAHOMYAI	540
Db	495	PFEANMPCII	PFYMMIHRSGCTSCFELEKICRFPMYSKXNYRVRPYNNMKXAVVAHOMYAI	554
QY	541	LÖNNNGLET	DEERKILLIACLCHLDHNGFSNSYLOKFDHPALALYSTSTMEQHHFSQTV	600
Db	555	LÖNNHTLET	DERKGLLIACLCHLDHNGFSNSYLOKFDHPALALYSTSTMEQHHFSQTV	614
QY	601	SILÖEGHNIF	STSLSSSEYEOVLIIIRKAIITADLAIYFNKRKÖLEBMVQTSGLMILNANS	660
Db	615	SILÖEGHNIF	STSLSSSEYEOVLIIIRKAIITADLAIYFNKRKÖLEBMVQTSGLMILNANS	674
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QY	781	APSKSTPE	788	
Db	795	AQKAASE	802	

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RESULT 3
US-09-686-055A-4
; Sequence 4, Application US/09686055A
; Patent No. 6566087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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LENGTH: 803  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-686-055A-4

Query Match 95.0%; Score 3997; DB 2; Length 803;  
 Best Local Similarity 95.4%; Pred. No. 0;  
 Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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75 NKSSEDESPKXSVSRVODTNMGVYELNSYLEORLDGDNHLLLYELSSIRIATKAD 134
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135 GPALATPLGECNNSLCVFIPPKMEGPRILIPAGPTTQGTISAVYAKSRKTLVLEDIGD 194
181 EFPFGTGESGTRIOSVCLPIVTAIGDLIGILEYRMGKEAPCLSHQEVATNLAWA 240
195 EFPFGTGESGTRIOSVCLPIVTAIGDLIGILEYRMGKEAPCLSHQEVATNLAWA 254
241 SVAIHQVQVCRGLAQTEINDFLLDVSKTYFDNIVAIDSLLEHIMIYAKLVNADRCALF 300
255 SVAIHQVQVCRGLAQTEINDFLLDVSKTYFDNIVAIDSLLEHIMIYAKLVNADRCALF 314
301 QVDHKKKELYSDFDIEGEEKGPRIFKTKETRFSEKGIAGQVATGVLNIPDAVYADP 360
315 QVDHKKKELYSDFDIEGEEKGPRIFKTKETRFSEKGIAGQVATGVLNIPDAVYADP 374
361 RRRREVDLTGTTTRNIIICMPIVSRGSLGVQVQWVKISGSAFSTKDDENNFKFAVFCAL 420
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421 ALHCANMYRIRHSECIYRVTEKLSYHSICTSEBQGLRPNLPARICRDIELFFHDIG 480
435 ALHCANMYRIRHSECIYRVTEKLSYHSICTSEBQGLRPNLPARICRDIELFFHDIG 494
481 PERNMMPGIFVYMIHRSCTGSCFELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAI 540
495 PERNMMPGIFVYMIHRSCTGSCFELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAI 554
541 LQNNHLLFTDLERKGLIACLDLHRRGFSNSYLQFDPHPLAALYSTMEQHHSQVY 600
555 LQNNHLLFTDLERKGLIACLDLHRRGFSNSYLQFDPHPLAALYSTMEQHHSQVY 614
601 SIQLEGHNIFFTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYOTGSLINLHNS 660
615 SIQLEGHNIFFTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYOTGSLINLHNS 674
661 HRDVIGLMWTACDLSVYTLMPVTKLTANDIYAEFAEGDEMKKGIQIPIPMDDPKD 720
675 HRDVIGLMWTACDLSVYTLMPVTKLTANDIYAEFAEGDEMKKGIQIPIPMDDPKD 734
721 EYVQGLGFNNAVAIPYTTLTQILPTEPLAKCRDNLNOMEKVLRGESTAMVSGPP 780
735 EYVQGLGFNNAVAIPYTTLTQILPTEPLAKCRDNLNOMEKVLRGESTAMVSGPP 794
781 APEKSTPE 788
795 AOKRAASE 802

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RESULT 4  
 US-08-951-648-6  
 Sequence 6, Application US/08951648  
 Patent No. 5933465  
 GENERAL INFORMATION:  
 APPLICANT: Loughney, Kate  
 TITLE OF INVENTION: Phosphodiesterase 8

NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker, Sears Tower Suite 6300  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: US  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/951,648  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Williams Jr., Joseph A.  
 REGISTRATION NUMBER: 38,659  
 REFERENCE/DOCKET NUMBER: 27866/34038  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-474-6300  
 TELEFAX: 312-474-0448  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 779 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-951-648-6

Query Match 92.2%; Score 3878; DB 1; Length 779;  
 Best Local Similarity 95.4%; Pred. No. 0;  
 Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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24 LNDERKAYALSLHPQVLDSESVSAETVEKMLKRKTAKADSPKXSVSRVODTNMG 83
14 LNDERKAYALSLHPQVLDSESVSAETVEKMLKRKNKSEDESPKXSVSRVODTNMG 73
84 VYELNSYLEORLDGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFIPPKMK 143
74 VYELNSYLEORLDGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFIPPKMK 133
144 EGQPRILIPAGPTTQGTISAVYAKSRKTLVLEDIGDEFPPGTTGLESSTRIOSVCLPI 203
134 EGQPRILIPAGPTTQGTISAVYAKSRKTLVLEDIGDEFPPGTTGLESSTRIOSVCLPI 193
204 VTAIGDLIGILEYRMGKEAPCLSHQEVATNLAWASVAIHQVQVCRGLAQTEINDFL 263
194 VTAIGDLIGILEYRMGKEAPCLSHQEVATNLAWASVAIHQVQVCRGLAQTEINDFL 253
264 LDVSKTYFDNIVAIDSLLEHIMIYAKLVNADRCALFOVDHKKKELYSDFDIEGEEKG 323
254 LDVSKTYFDNIVAIDSLLEHIMIYAKLVNADRCALFOVDHKKKELYSDFDIEGEEKG 313
324 PIFFKTKETRFSEKGIAGQVARTGVLNIPDAVADPRRRREVDLTGTTTRNIIICMPIY 383
314 PIFFKTKETRFSEKGIAGQVARTGVLNIPDAVADPRRRREVDLTGTTTRNIIICMPIY 373
384 SRGSLGVQVQWVKISGSAFSTKDDENNFKFAVFCALALHCANMYRIRHSECIYVTE 443
374 SRGSLGVQVQWVKISGSAFSTKDDENNFKFAVFCALALHCANMYRIRHSECIYVTE 433
444 KLSYHSICTSEBQGLRPNLPARICRDIELFFDIEGPEENMMPGIFVYMIHRSCTGSCF 503
434 KLSYHSICTSEBQGLRPNLPARICRDIELFFDIEGPEENMMPGIFVYMIHRSCTGSCF 493
504 ELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAILQNNHLLFTDLERKGLIACLDCH 563
494 ELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAILQNNHLLFTDLERKGLIACLDCH 553
564 DLHRRGFSNSYLQFDPHPLAALYSTMEQHHSQVTSIQLGEGHNIFFTLSSSEYEQVL 623

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Db 554 DLDHGFNSYLOQRDHPALALYSTWEOHHFSGTWSILOEGHNIFSTLSSSEYEQVL 613  
Qy 624 EIRKAIITATDALYFGNRKOLEEMVQTSGLNHQSHDRVIGLMTACDLCSTYKLP 683  
Db 614 EIRKAIITATDALYFGNRKOLEEMVQTSGLNHQSHDRVIGLMTACDLCSTYKLP 673  
Qy 664 VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743  
Db 674 VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 733  
Qy 744 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778  
Db 734 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778  
RESULT 5  
US-09-174-437-6  
; Sequence 6, Application US/09174437A  
; Patent No. 6133007  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/174,437A  
; CURRENT FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 08/951,648  
; EARLIER FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 779  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-174-437-6

Query Match 92.2%; Score 3878; DB 2; Length 779;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 24 LTDEKVKAYLSLHPVLDLDFVSESVSAETVEKMLKRTNKAKDESPKESVRYODTNMG 83  
Db 14 LTDEKVKAYLSLHPVLDLDFVSESVSAETVEKMLKRTNKAKDESPKESVRYODTNMG 73  
Qy 84 VVYEINSLYIEQRLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFLPQMK 143  
Db 74 VVYEINSLYIEQRLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFLPQMK 133  
Qy 144 EGQPLIPAGPITGOTTISAVYAKSRKTLVBDLIGDERFRPGTGLESTRIOSTVLCPI 203  
Db 134 EGQPLIPAGPITGOTTISAVYAKSRKTLVBDLIGDERFRPGTGLESTRIOSTVLCPI 193  
Qy 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANLMAVAIHQOVCGRLAQTEINDFL 263  
Db 194 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANLMAVAIHQOVCGRLAQTEINDFL 253  
Qy 264 LDVSKTYFDNIYALDSLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKXGK 323  
Db 254 LDVSKTYFDNIYALDSLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKXGK 313  
Qy 324 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFRNREVDLYTGTTRNIIICMPIV 383  
Db 314 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFRNREVDLYTGTTRNIIICMPIV 373  
Qy 384 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAHYHRIHSECIYRYTME 443  
Db 374 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAHYHRIHSECIYRYTME 433  
Qy 444 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRHSGTSCF 503  
Db 434 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRHSGTSCF 493  
Qy 504 ELKLCRFIMSKYKQYRVRPHYNNMKHAYTVAHCMVAIIQNNNGLFTDLBRKGLLACLGCH 563

Db 494 ELKLCRFIMSKYKQYRVRPHYNNMKHAYTVAHCMVAIIQNNNGLFTDLBRKGLLACLGCH 553  
Qy 564 DLDHGFNSYLOQRDHPALALYSTWEOHHFSGTWSILOEGHNIFSTLSSSEYEQVL 623  
Db 554 DLDHGFNSYLOQRDHPALALYSTWEOHHFSGTWSILOEGHNIFSTLSSSEYEQVL 613  
Qy 624 EIRKAIITATDALYFGNRKOLEEMVQTSGLNHQSHDRVIGLMTACDLCSTYKLP 683  
Db 614 EIRKAIITATDALYFGNRKOLEEMVQTSGLNHQSHDRVIGLMTACDLCSTYKLP 673  
Qy 664 VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743  
Db 674 VTKLTIANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 733  
Qy 744 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778  
Db 734 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778

RESULT 6  
US-09-686-055A-6  
; Sequence 6, Application US/09686055A  
; Patent No. 6566087  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/686,055A  
; CURRENT FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 08/951,648  
; PRIOR FILING DATE: 1997-10-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 779  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-686-055A-6

Query Match 92.2%; Score 3878; DB 2; Length 779;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 24 LTDEKVKAYLSLHPVLDLDFVSESVSAETVEKMLKRTNKAKDESPKESVRYODTNMG 83  
Db 14 LTDEKVKAYLSLHPVLDLDFVSESVSAETVEKMLKRTNKAKDESPKESVRYODTNMG 73  
Qy 84 VVYEINSLYIEQRLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFLPQMK 143  
Db 74 VVYEINSLYIEQRLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFLPQMK 133  
Qy 144 EGQPLIPAGPITGOTTISAVYAKSRKTLVBDLIGDERFRPGTGLESTRIOSTVLCPI 203  
Db 134 EGQPLIPAGPITGOTTISAVYAKSRKTLVBDLIGDERFRPGTGLESTRIOSTVLCPI 193  
Qy 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANLMAVAIHQOVCGRLAQTEINDFL 263  
Db 194 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANLMAVAIHQOVCGRLAQTEINDFL 253  
Qy 264 LDVSKTYFDNIYALDSLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKXGK 323  
Db 254 LDVSKTYFDNIYALDSLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKXGK 313  
Qy 324 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFRNREVDLYTGTTRNIIICMPIV 383  
Db 314 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFRNREVDLYTGTTRNIIICMPIV 373  
Qy 384 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAHYHRIHSECIYRYTME 443  
Db 374 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAHYHRIHSECIYRYTME 433  
Qy 444 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRHSGTSCF 503

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Db      424 KLSYHSICTSEEMOGLMFTLPVRLCKEILFHPDIPGPENNMPCI FYVMVHRSCTGSCF 493
Qy      504 ELEKLCRFMSYKQYRRVPYNNMKAIVVAHCMTAIIQNNNGLFTDLERKGLIACLC 563
Db      494 ELEKLCRFMSYKQYRRVPYNNMKAIVVAHCMTAIIQNNNGLFTDLERKGLIACLC 553
Qy      564 DLDHGFNSYLOKFDHPALALYSTSTMEQHHSQTVSIIQLEGNHIFSTLSSSEYEQVL 623
Db      554 DLDHGFNSYLOKFDHPALALYSTSTMEQHHSQTVSIIQLEGNHIFSTLSSSEYEQVL 613
Qy      624 EIRRAIATDIALYFGNRKQLEEMVQGTSLINLNNQSHRDVIGLMTACDLCSTYKLP 683
Db      614 EIRRAIATDIALYFGNRKQLEEMVQGTSLINLNNQSHRDVIGLMTACDLCSTYKLP 673
Qy      684 VTKLITANDIYAEFWABGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLTQ 743
Db      674 VTKLITANDIYAEFWABGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLTQ 733
Qy      744 ILPTEPLKACRDNLQWMEKVI RGETAMWISGPGAPAPSKSTPE 788
Db      734 ILPTEPLKACRDNLQWMEKVI RGETAMWISGPGAPAPSKSTPE 778

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RESULT 7
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. 6673564
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methode for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

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Query Match 92.2%; Score 3878; DB 2; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy      24 LTDEKVAAYSLHPQVLDSEFVSSESAETVEKMLKRTNRAKDESPKESRYQDTMVG 83
Db      14 LTDEKVAAYSLHPQVLDSEFVSSESAETVEKMLKRTNRAKDESPKESRYQDTMVG 73
Qy      84 VVEELNSYIEQRDLDTGDNHLLVYELSSIIIRIATKADGPAIYFEGCNNSLCYFIIPGMK 143
Db      74 VVEELNSYIEQRDLDTGDNHLLVYELSSIIIRIATKADGPAIYFEGCNNSLCYFIIPGMK 133
Qy      144 EGQPRILPAPPIYQGTITSAVNAKSRTLLVEDLGBERPRRGESGRIRIOSVLCPLI 203
Db      134 EGQPRILPAPPIYQGTITSAVNAKSRTLLVEDLGBERPRRGESGRIRIOSVLCPLI 193
Qy      204 VTAIGDLIGILELRHNGKEAFCLSHQEVATANLAMSVAIHQVQCRGLAKQTELNDPL 263
Db      194 VTAIGDLIGILELRHNGKEAFCLSHQEVATANLAMSVAIHQVQCRGLAKQTELNDPL 253
Qy      264 LDVSKTYFDNIIVADSLLEHIMYAKULVNADRCALFQVDHKNKELYSDFDIGEEKGK 323
Db      254 LDVSKTYFDNIIVADSLLEHIMYAKULVNADRCALFQVDHKNKELYSDFDIGEEKGK 313
Qy      324 PIKKTEIRPSTIRKGIAGQVAFGEVLTNPDAVADPRNREVDLYGTYTRNLCPPIV 383
Db      314 PIKKTEIRPSTIRKGIAGQVAFGEVLTNPDAVADPRNREVDLYGTYTRNLCPPIV 373

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Qy      384 SRGSIVGVQWVWKISGSAFSTDENNKMPAVFCALALHCANMYHRIHSECIYRTME 443
Db      374 SRGSIVGVQWVWKISGSAFSTDENNKMPAVFCALALHCANMYHRIHSECIYRTME 433
Qy      444 KLSYHSICTSEEMOGLMFPNIPARICDI ELFHPDIPGPENNMPCI FYVMHRSCTGSCF 503
Db      434 KLSYHSICTSEEMOGLMFTLPVRLCKEILFHPDIPGPENNMPCI FYVMVHRSCTGSCF 493
Qy      504 ELEKLCRFMSYKQYRRVPYNNMKAIVVAHCMTAIIQNNNGLFTDLERKGLIACLC 563
Db      494 ELEKLCRFMSYKQYRRVPYNNMKAIVVAHCMTAIIQNNNGLFTDLERKGLIACLC 553
Qy      564 DLDHGFNSYLOKFDHPALALYSTSTMEQHHSQTVSIIQLEGNHIFSTLSSSEYEQVL 623
Db      554 DLDHGFNSYLOKFDHPALALYSTSTMEQHHSQTVSIIQLEGNHIFSTLSSSEYEQVL 613
Qy      624 EIRRAIATDIALYFGNRKQLEEMVQGTSLINLNNQSHRDVIGLMTACDLCSTYKLP 683
Db      614 EIRRAIATDIALYFGNRKQLEEMVQGTSLINLNNQSHRDVIGLMTACDLCSTYKLP 673
Qy      684 VTKLITANDIYAEFWABGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLTQ 743
Db      674 VTKLITANDIYAEFWABGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLTQ 733
Qy      744 ILPTEPLKACRDNLQWMEKVI RGETAMWISGPGAPAPSKSTPE 788
Db      734 ILPTEPLKACRDNLQWMEKVI RGETAMWISGPGAPAPSKSTPE 778

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RESULT 8
US-08-951-648-2
; Sequence 2, Application US/08951648
; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker, Sears Tower Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: /note= "The amino acid at position 290 is either Pro
; OTHER INFORMATION: or Leu."
US-08-951-648-2

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Query Match 92.1%; Score 3873; DB 1; Length 766;

Best Local Similarity 95.3%; Pred. No. 0;  
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 24 LTDEKVAYLISHLPQVLDFEVSSESAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 83
DB 1 LTDEKVAYLISHLPQVLDFEVSSESAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 60
QY 84 VVEELNSYIEQRLDGDNHLLLYELSSIIIRIATKADGPAFLYFGECCNSLCVFPFPGMK 143
DB 61 VVEELNSYIEQRLDGDNHLLLYELSSIIIRIATKADGPAFLYFGECCNSLCVFPFPGIK 120
QY 144 EGQPLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSEGTRIQSVCPLPI 203
DB 121 EGQPLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSEGTRIQSVCPLPI 180
QY 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 263
DB 181 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 240
QY 264 LDVSKTYPDNIYALDSLEHIMITYAKNLVNAIDRCALFQVDHKNKELYSDFDIGEEKGK 323
DB 241 LDVSKTYPDNIYALDSLEHIMITYAKNLVNAIDRCALFQVDHKNKELYSDFDIGEEKGK 300
QY 301 PVFKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNEVDLYTGYTTRNIIICMPIV 360
DB 301 PVFKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNEVDLYTGYTTRNIIICMPIV 360
QY 364 SRGSVIGVQVQVNNKISGSAFSKTDENNFKMPFAVFCALAHCANMYHRIHSECIYRVME 443
DB 361 SRGSVIGVQVQVNNKISGSAFSKTDENNFKMPFAVFCALAHCANMYHRIHSECIYRVME 420
QY 444 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPEMMWPGIFVYMHRSCTSCF 503
DB 421 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPEMMWPGIFVYMHRSCTSCF 480
QY 504 ELEKLCRFIMSVKQYRVRPYHNMKHAVTVAHCMYAILQNNNGHFTDLERKGLIACLCCH 563
DB 481 ELEKLCRFIMSVKQYRVRPYHNMKHAVTVAHCMYAILQNNNGHFTDLERKGLIACLCCH 540
QY 564 DLDHGFNSSYLQKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYEQVL 623
DB 541 DLDHGFNSSYLQKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYEQVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNHNQSHRDVIGLMMTACDLCSVTKLMP 683
DB 601 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNHNQSHRDVIGLMMTACDLCSVTKLMP 660
QY 684 VTKLTANDIYAEFMAEGDEMKGIGIOPIPMDRDKDEVPQOGLGFYNAVAIPCTYTLITQ 743
DB 661 VTKLTANDIYAEFMAEGDEMKGIGIOPIPMDRDKDEVPQOGLGFYNAVAIPCTYTLITQ 720
QY 744 ILPTEPLIKACRDNLNQWEKVIIRGEETAMWISGPGAPSKSTPE 788
DB 721 ILPTEPLIKACRDNLNQWEKVIIRGEETAMWISGPGAPSKSTPE 765
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RESULT 9  
US-09-174-437-2  
; Sequence 2, Application US/09174437A  
; Patent No. 6133007  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/174,437A  
; EARLIER FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 08/951,648  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 766  
; TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (274)  
; OTHER INFORMATION: The amino acid is either Pro or Leu  
US-09-174-437-2

Query Match 92.1%; Score 3873; DB 2; Length 766;  
Best Local Similarity 95.3%; Pred. No. 0;  
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 24 LTDEKVAYLISHLPQVLDFEVSSESAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 83
DB 1 LTDEKVAYLISHLPQVLDFEVSSESAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 60
QY 84 VVEELNSYIEQRLDGDNHLLLYELSSIIIRIATKADGPAFLYFGECCNSLCVFPFPGMK 143
DB 61 VVEELNSYIEQRLDGDNHLLLYELSSIIIRIATKADGPAFLYFGECCNSLCVFPFPGIK 120
QY 144 EGQPLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSEGTRIQSVCPLPI 203
DB 121 EGQPLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSEGTRIQSVCPLPI 180
QY 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 263
DB 181 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 240
QY 264 LDVSKTYPDNIYALDSLEHIMITYAKNLVNAIDRCALFQVDHKNKELYSDFDIGEEKGK 323
DB 241 LDVSKTYPDNIYALDSLEHIMITYAKNLVNAIDRCALFQVDHKNKELYSDFDIGEEKGK 300
QY 301 PVFKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNEVDLYTGYTTRNIIICMPIV 360
DB 301 PVFKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNEVDLYTGYTTRNIIICMPIV 360
QY 364 SRGSVIGVQVQVNNKISGSAFSKTDENNFKMPFAVFCALAHCANMYHRIHSECIYRVME 443
DB 361 SRGSVIGVQVQVNNKISGSAFSKTDENNFKMPFAVFCALAHCANMYHRIHSECIYRVME 420
QY 444 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPEMMWPGIFVYMHRSCTSCF 503
DB 421 KLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIGPEMMWPGIFVYMHRSCTSCF 480
QY 504 ELEKLCRFIMSVKQYRVRPYHNMKHAVTVAHCMYAILQNNNGHFTDLERKGLIACLCCH 563
DB 481 ELEKLCRFIMSVKQYRVRPYHNMKHAVTVAHCMYAILQNNNGHFTDLERKGLIACLCCH 540
QY 564 DLDHGFNSSYLQKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYEQVL 623
DB 541 DLDHGFNSSYLQKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYEQVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNHNQSHRDVIGLMMTACDLCSVTKLMP 683
DB 601 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNHNQSHRDVIGLMMTACDLCSVTKLMP 660
QY 684 VTKLTANDIYAEFMAEGDEMKGIGIOPIPMDRDKDEVPQOGLGFYNAVAIPCTYTLITQ 743
DB 661 VTKLTANDIYAEFMAEGDEMKGIGIOPIPMDRDKDEVPQOGLGFYNAVAIPCTYTLITQ 720
QY 744 ILPTEPLIKACRDNLNQWEKVIIRGEETAMWISGPGAPSKSTPE 788
DB 721 ILPTEPLIKACRDNLNQWEKVIIRGEETAMWISGPGAPSKSTPE 765
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RESULT 10  
US-09-686-055A-2  
; Sequence 2, Application US/09686055A  
; Patent No. 656087  
; GENERAL INFORMATION:  
; APPLICANT: Loughney, Kate  
; TITLE OF INVENTION: Phosphodiesterase 8A  
; FILE REFERENCE: 27866/35047  
; CURRENT APPLICATION NUMBER: US/09/686,055A

;; CURRENT FILING DATE: 2000-10-11  
;; PRIOR APPLICATION NUMBER: 08/951,648  
;; PRIOR FILING DATE: 1997-10-16  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 2  
;; LENGTH: 766  
;; TYPE: prt  
;; ORGANISM: Homo sapiens  
;; NAME/KEY: misc feature  
;; LOCATION: (290)  
;; OTHER INFORMATION: The amino acid is either Pro or Leu  
US-09-686-055A-2

Query Match 92.1%; Score 3873; DB 2; Length 766;  
Best Local Similarity 95.3%; Pred. No. 0;  
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 24 LTDEKVKAYLSHPQVLDFEVSASAEVVEKMLKRTKAKADEPPEKVSRYQDTNMG 83
DB 1 LTDEKVKAYLSHPQVLDFEVSASAEVVEKMLKRTKAKADEPPEKVSRYQDTNMG 60
QY 84 VYELNSYIEQRIDTGDNDHLLYELSSIIIRIATKADGPAFLYELGSCNLSLCTFIPGAK 143
DB 61 VYELNSYIEQRIDTGDNDHLLYELSSIIIRIATKADGPAFLYELGSCNLSLCTFIPGAK 120
QY 144 EGGPRLIPAGPIQTGTTISAVYAKSRKTLVEDILDERFPRTGLESSTRLOSVLCP1 203
DB 121 EGGPRLIPAGPIQTGTTISAVYAKSRKTLVEDILDERFPRTGLESSTRLOSVLCP1 180
QY 204 VTAIGDLIGILELYRMKKEAFLSHQEVATANLANASVAIHQVYCRGLAKOTELNDPL 263
DB 181 VTAIGDLIGILELYRMKKEAFLSHQEVATANLANASVAIHQVYCRGLAKOTELNDPL 240
QY 264 LDVSKTYFPDNIYVADSLSEHIMYAKLVNADRCALFOVDHKKELYSDFDGEKEGK 323
DB 241 LDVSKTYFPDNIYVADSLSEHIMYAKLVNADRCALFOVDHKKELYSDFDGEKEGK 300
QY 324 PIKTKTEIRFSEIEKGIAGVARTGEVANI PDAYADPRFREVLYTGYTTRN1LCP1Y 383
DB 301 PIKTKTEIRFSEIEKGIAGVARTGEVANI PDAYADPRFREVLYTGYTTRN1LCP1Y 360
QY 384 SRGSGVIGVOMVKKISGSASFSTKDENNFKMFAYFCALALHCAAMYHRIHSECIYRVTME 443
DB 361 SRGSGVIGVOMVKKISGSASFSTKDENNFKMFAYFCALALHCAAMYHRIHSECIYRVTME 420
QY 444 KLSYHSICTSEEWQGLMRPNLPARICDILFHFIDICPFENMFGIYVYMIHSCGTSFC 503
DB 421 KLSYHSICTSEEWQGLMRPNLPARICDILFHFIDICPFENMFGIYVYMIHSCGTSFC 480
QY 504 ELEKLCGFIMSVKKNYRVRVYHNMKHAVTVAHCVATL1LNNNGLFDTLBERKGLLIACLC 563
DB 481 ELEKLCGFIMSVKKNYRVRVYHNMKHAVTVAHCVATL1LNNNGLFDTLBERKGLLIACLC 540
QY 564 DLDRHGSNSYLQKFDHPLAALYSTSTMBQHHFSQVYS1LQLEBGN1FSTLSSESEYQVL 623
DB 541 DLDRHGSNSYLQKFDHPLAALYSTSTMBQHHFSQVYS1LQLEBGN1FSTLSSESEYQVL 600
QY 624 EIRIKAL1ATDLALYFGNRKQLEEMVYOTGSLANLNQSHRDVIGLMMTACDLC5VTGLMP 683
DB 601 EIRIKAL1ATDLALYFGNRKQLEEMVYOTGSLANLNQSHRDVIGLMMTACDLC5VTGLMP 660
QY 684 VTKLTANDIYAEFAEAGDEMKKLG1OPI PMMDRDKRBEVPOGOLGAFYNAVA1PCYTTLTLO 743
DB 661 VTKLTANDIYAEFAEAGDEMKKLG1OPI PMMDRDKRBEVPOGOLGAFYNAVA1PCYTTLTLO 720
QY 744 ILPTEPL1KACRDNLNOMKEVIRIGEETAMWISGPGAPASKSTPE 788
DB 721 ILPTEPL1KACRDNLNOMKEVIRIGEETAMWISGPGAPASKSTPE 765
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RESULT 11  
US-10-296-144-5

;; Sequence 5, Application US/10296144  
;; Patent No. 6919185  
;; GENERAL INFORMATION:  
;; APPLICANT: Bayer AG  
;; TITLE OF INVENTION: REGULATION OF HUMAN TRANSKETOLASE-LIKE ENZYME  
;; FILE REFERENCE: 140078  
;; CURRENT APPLICATION NUMBER: US/10/296,144  
;; PRIOR FILING DATE: 2002-11-22  
;; PRIOR APPLICATION NUMBER: 60/207,950  
;; PRIOR FILING DATE: 2000-05-31  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 1284  
;; TYPE: prt  
;; ORGANISM: Drosophila melanogaster  
US-10-296-144-5

Query Match 24.0%; Score 1010; DB 2; Length 1284;  
Best Local Similarity 32.7%; Pred. No. 4,88-97;  
Matches 248; Conservative 143; Mismatches 280; Indels 88; Gaps 18;

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QY 70 PKVSR--YQDTNMOGVYELNSYIEQRIDTGDNDHLLYELSSIIIRIATKADGPAFLYL 127
DB 197 PKRLSRNKLQDKEKELIFELVKD1CNELEVRTLCCHK1LQNVSS---1L1NADRGSLFLV 252
QY 128 -GECNNSLCVF1PPEKKEG-QRRLIPAGP-----1TGGTTISAVYAKSRKT 171
DB 253 QGRKNG-----PDG1KKCLVSKLFDVCPSTVEENQODEVRVWAGT1AGHVAHSGEP 306
QY 172 LVEDILDERFPRTGLESSTRLOSVLCTPIVTAIGDLIGILELYRMKKEAFLSHQEV 231
DB 307 VNIIPDYQDERFRC1DLSITGYRTAL1LCP1KDSGSDV1GVAQV1NKNNGEFS1D1EK 366
QY 232 VATANLANASVAIHQVYCRGLAKOTELNDPLDVSKTYFPDNIYVADSLSEHIMYAKLV 291
DB 367 VSSSYLQFCGIG1GRNMQ1LEKSGLEIKRNOVL1DLARM1FEQST1EHNVFRL1TMO1SI 426
QY 292 VNADRCALFOVDHKKELYSDF-----DIGEKEGKPIPKTK--EIRFSEKGIAGV 344
DB 427 IQCORVQI1LVHEADKGSF5RVDFEANDLSBBE---ATSRSPYESSRP1NIGITGHV 482
QY 345 ARPGEVLAN1PDYADPRFREVLYTGYTTRN1LCP1Y-SRGSGVIGVOMVKKISGSASF 403
DB 483 ATGGETVNPNAVEDR1FPA5VDENS1CFKGR1SL1CAL1KNS1DQ11GV1OL1NKRE1LDF 542
QY 404 SKTDENNFOMFAVFCALALHCAAMYHRIHSECIYRVTMEKLSYHSICTSEEWQGL----- 459
DB 543 TKNDENFVFA1FCMG1HNTMYEKATVAMAKQSVTL1EVS1YHSA1TMD1EAB1RLRKQK 602
QY 460 -----MRPNLPARICDILFHFIDICPFEN-----MMPG 488
DB 603 QQQQAVGLRQAP1SLPPRK1LQRL1RVP1SAVH1RLAD1F1FDD1DTL1KAC1LRF1LD 662
QY 489 1-FVYMIHSCGTSCELEKLCGFIMSVKKNYRVRVYHNMKHAVTVAHCVATL1LNNNG 545
DB 663 LDFVERFH-----IDYEVLCRW1L1SVKKNYRVRVYHNMKHAVTVAHCVATL1LNNNG 715
QY 546 GLFTDLBERKGLLIAC1CHD1DRHGSNSYLQKFDHPLAALYSTSTMBQHHFSQVYS1LQ 605
DB 716 KITGE1ECLAL1IG1CLCHD1DRHGTNNS1FO1KXSS1PLAQ1YSTSTMBQHHFSQVYS1LQ 775
QY 606 EGNH1FSTLSSESEYQVLE1IRKAL1ATDLALYFGNRKQ-LEEMVYOTGSLANLNQSHRDR 664
DB 776 RGNQ1LIANSSDDY1CRV1RVL1EDAL1STDLAV1FKK1G1P1LESVSQ1TSYVAB1BP-1AL 834
QY 665 VIGLMMTACDLC5VTGLMP1TK1TANDIYAEFAEAGD-EKK1G1OPI1PMMDRDKRBEV 723
DB 835 1RAM1MTV1CDLS1AT1YK1WE1EK1RVAD1VS1E1FEQ1G1MEK1Q1BN1T1F1D1N1REK1ED1LP 894
QY 724 QGOLGAFYNAVA1PCYTTLTLO1LPTEPL1KACRDNLNOM 762
DB 895 MMQVNF1DS1CLP1YE1FA1LSD1K1E1PLV1G1VAD1NRGHM 933
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```

RESULT 12
US-08-480-547A-10
/ Sequence 10, Application US/08480547A
/ Patent No. 5652131
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Corbin, Jackie D.
/ APPLICANT: Ferguson, Kenneth M.
/ APPLICANT: Francis, Sharon H.
/ APPLICANT: Kadlecsek, Ann
/ APPLICANT: Loughney, Kate
/ APPLICANT: McAllister-Lucas, Linda M.
/ APPLICANT: Sonnenburg, William K.
/ APPLICANT: Thomas, Melissa K.
/ TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
/ TITLE OF INVENTION: Phosphodiesterase Materials and Methods
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,547A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5652131and, Greca E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 32791
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 875 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-480-547A-10

Query Match      21.8%; Score 918; DB 1; Length 875;
Best Local Similarity 30.2%; Pred. No. 1.4e-87;
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

QY 10 SCFRRLTEGFLSPSLTDE-----KYKAY---LSLHPVLDE-----FVSSVSXAE 51
DB 68 SC-----SCPLDPSPPRESSVPGTPTRKISABEPRLPRIVYKDSGTVSFLSDSKKE 122
QY 52 TVEKWLKRTNKAKDEPSPKEVSRVQDTNMCGVVEELNSYIEQRDLDTGDNHLLLEYELSS 111
DB 123 QMPRLSPRDNDEGQCSR-----LLELVNDISHDVTLCKHIFLHNG 168
QY 112 IIRIATKADGFLYPLGECNSNLGVFIIPGMEKGQRLIPAGPIQGT----- 160
DB 169 LI-----SADRYSLFLVCEBDSNDKFLI-----SLPL-----DVAEGSTLEBASNNCIRL 213
QY 161 -----ISAVASRKTLVLEDILSDERFRGTGLSSGTRIGSVLCLPIYTAIGDLIGILE 215
DB 214 EWNKGIIVGVAAFGSEPLNKDAVEDPRFAAEVDQITGYTOSILCMPIKNHREEVGVAAQ 273
QY 216 LY--BHWGKEAFCLSHOEVAATNLAMASVAIHQVQVCRGIAQTEINDELVDVSKTYFPDN 273

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DB 274 AINKSGNGCTFEKDEKOPAAVLAFCGIVLNMQLYETSLLENKRNQVLLDLASLIFEE 333
QY 274 IVAIDSLIEHIMITAKNLVNBDRCALFOVDHKNKELYSDLPDIGEKEXDPIPKTKIEIR 333
DB 334 QOSELVILKKTIAATISPMQVOKCTIFVDEDCSDSFSSVTHMECELEKESDITLRERD 393
QY 334 FS-IEKGIAGQVARTGEVLANIPDAYADPRF--NREVDLYGTYTRNLLCMPIYS--RGS 387
DB 394 ANRIWYMYAQVYKNTMEPLNIPDYSKDRFPMTENMGNINQOCIRSLCTPIKNGKXK 453
QY 368 VIGVQVQVNTKISGS-----AFSKTDENNFKMPAYFCALALCANNYHRIHSECIYRTM 442
DB 454 VIGVQVQVNTKISGS-----AFSKTDENNFKMPAYFCALALCANNYHRIHSECIYRTM 442
QY 443 EKLSTYHSICTSEEMOGMLRNFULPARI-----CRDIELFHPDIPGPNMMPGIFVYMI 494
DB 514 EULSTYHASAABEETRELO--SLAAVPSAQTCLKTDTSPDSFDELSDLETALCTIRMTD 571
QY 495 HRSCTSCFELEKLCRFYMSYKQVYR--VPYHNMKAVTVAHCMYALQNN--NGLFTDL 551
DB 572 LNIYQNPQMKHEVLCKWILSVKQYRKVAHYHNRHAFNTAQCMFPAALKAQKIQKRLTDL 631
QY 552 ERKGLIACLDHDDHRCFSNSYQKFDPIALALYSTIMEQHFSQTVSILQEGHNIIF 611
DB 632 BILALLIALSHDDHRCVNSYIORSSEHPLAOLYCHSIMEHHHPDQCLMILNSPQOIL 691
QY 612 STLSSEVEQVLEITRKAITATDIALYFGNRKOLEEMVQTSILNHNQSHRDVIGLMMT 671
DB 692 SGLSTEEYKTKTLTKKALATDIALYKRGSEFELMKQNFQIEDHQKELFIAMLT 751
QY 672 ACDLCSYTKLMPVTGLTANDIYAEFWAGD--EMKKLGIOPIPMMDRDRDEVPQQLGFY 730
DB 752 ACDLSAITEKPIQORIALVATEFPDGDGRERKEINIEPADLNNREKKNIPSMQVQFI 811
QY 731 NAVAIPCTYTLTQILPPEPLIKACRDNLNQMEKVIRGEETAMISG 777
DB 812 DAICIQLEYALTHVSEDCFPILDGCRKNRKQKQALAEQOETKL-ING 857

RESULT 13
US-08-250-847B-10
/ Sequence 10, Application US/08250847B
/ Patent No. 5702936
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Corbin, Jackie D.
/ APPLICANT: Ferguson, Kenneth M.
/ APPLICANT: Francis, Sharon H.
/ APPLICANT: Kadlecsek, Ann
/ APPLICANT: Loughney, Kate
/ APPLICANT: McAllister-Lucas, Linda M.
/ APPLICANT: Sonnenburg, William K.
/ APPLICANT: Thomas, Melissa K.
/ TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
/ TITLE OF INVENTION: Phosphodiesterase Materials and Methods
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/250,847B
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:

```



APPLICATION NUMBER: US 08/068,051  
FILING DATE: 27-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5702936and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 875 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-250-847B-10

Query Match 21.8%; Score 918; DB 1; Length 875;  
Best Local Similarity 30.2%; Pred. No. 1.4e-87;  
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

10 SCFRRLTECFLSLTD-----KXAY---LSLHPQLD-----FVSEVSAR 51  
68 SC-----SCPLQSPRAESSVPPTPRKISASEFDRPLRPVYKDSGTVSFLSDSKCE 122  
52 TVEKMLKRTNKADESPPEVSRVQDTMNGVYVELNSYIEORLDTGDNHLLVLELSS 111  
123 QMPLTSPFRDNDGDCSR-----LLELVNDISSHLVLTALCHKIFLHIHG 168  
112 IIRIATKADGAFALYFGECNNSLCVPIPGMKEGOPRLIPAGPITQGT----- 160  
169 LI-----SADRYSLFLVCEDSSNDKFLI-----SRLF---DVAEGSTLEASNNCIRL 213  
161 -----ISAVYASRKTLVLEDILGDRFRPGTGESTRIGSTLCPIYALGDLGILE 215  
214 ENKKGIVGVAAGPEPLNTKDAYEDPRFAAEVDQITGYKQSTLCMPIKNREEVGVAAO 273  
216 LV--RHMGEAFCLSHOEVAATNLAASVAVIHQVQCRGLAKOTELNDPLLDVSKTYFDN 273  
274 AINKSGNGSTFEKKEKOPAYLACGIVLHNAQLETSLKNGNOVLDDASLILFEE 333  
274 IYVADLSLEHIMIVAKLVNADRCALFOVDHKNKELYSDFDICEKEGKPIFKTEIR 333  
334 QGSEVLTLKKIATITISPMQVQCTIFIVDEDCSFSVYHMECEBELKESDTLIREHD 393  
334 PS-IEKGIAQVARTGEVLNIPRAYADPR--NREVDLYTGTTNIIICMPIVS--RGS 387  
394 ANRINMYAQYVKNTEPLNIPVSKDKRPPWTNENNGINQOCIRSLCTPIKNGKXK 453  
388 VIGVGVNVNKSIS-----AFSKTDENNFGFAVFCALALHCANMYRIRHSECIYVTM 442  
454 VIGVGVNVNMEETGGKVAFAFNDEQFLFAVIFCGLGQNTOMTEAVRAAKAKQVTL 513  
443 EKLSYHSICTSEEMOGIMRPNLPARI-----CRDIELFHPDIGFFENMWPGIFVYMI 494  
514 EYLSYHSAABEETRELQ--SLAAVVPQAOTLKITDFFSDPELSDELTAICTIRAFED 571  
495 HNSCGTSCPELEKLCRFIMSVKKNYR--VPIYNNKCAVNTVAHCAVIALONN--NGLEFDTL 551  
572 LNVQFQMGHGEVLCVKILSVKKNYRKNVAYHNRHAFNTAOCMFALKKGKIQKRLTDL 631  
552 ERKGLLIACCHLDHGRGFSNLYOKEDHPALALYSTTMEOHNFSTQVSILOLEGNIF 611  
632 EYIALTLALSHDHRGVNNSYIQSEHPLAOLYCHSIMEHHFPOCLMILNSPQOIL 691  
612 STLSSEYEEVLEIRKAIATDVALYFGNRKOLEMYQTSGLNHLNQSHRDVIGLMT 671  
692 SGLSIEBYKTKTKIKQAILATDVALYIKRGEFFELIMKNQFALBPHOKELFLAMLT 751  
672 ACULCSTYKMPYTKLTANDIYAFNAEGD-EMKGLGIQPIPMMDRKRQREVPQSGLGFY 730  
752 ACULSALTQKMPIQORLAEIVATEFPQDGRERKELNIBPADLNKREKKNKIPSMQVGF 811

731 NAVAIPCTYTLTQILPTEPILKACRDNLNOMEKVIIRGETAMWISG 777  
812 DAICQLVETLHVSEDCFPILDDGCRKNRQKQWALABQOEKTL-ING 857

RESULT 14  
US-08-463-949A-10  
Sequence 10, Application US/08463949A  
Patent No. 5955583  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Corbin, Jackie D.  
APPLICANT: Ferguson, Kenneth M.  
APPLICANT: Francis, Sharon H.  
APPLICANT: Kadlecsek, Ann  
APPLICANT: Loughney, Kate  
APPLICANT: McAllister-Lucas, Linda M.  
APPLICANT: Sonnenburg, William K.  
APPLICANT: Thomas, Melissa K.  
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific  
TITLE OF INVENTION: Phosphodiesterase Materials and Methods  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 213 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,949A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/068,051  
FILING DATE: 27-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5955583and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32706  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 875 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-949A-10

Query Match 21.8%; Score 918; DB 1; Length 875;  
Best Local Similarity 30.2%; Pred. No. 1.4e-87;  
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

10 SCFRRLTECFLSLTD-----KXAY---LSLHPQLD-----FVSEVSAR 51  
68 SC-----SCPLQSPRAESSVPPTPRKISASEFDRPLRPVYKDSGTVSFLSDSKCE 122  
52 TVEKMLKRTNKADESPPEVSRVQDTMNGVYVELNSYIEORLDTGDNHLLVLELSS 111  
123 QMPLTSPFRDNDGDCSR-----LLELVNDISSHLVLTALCHKIFLHIHG 168  
112 IIRIATKADGAFALYFGECNNSLCVPIPGMKEGOPRLIPAGPITQGT----- 160  
169 LI-----SADRYSLFLVCEDSSNDKFLI-----SRLF---DVAEGSTLEASNNCIRL 213

[illegible]

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,410A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6037119and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32705
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-410A-10

Query Match      21.8%; Score 918; DB 2; Length 875;
Best Local Similarity 30.2%; Pred. No. 1,4e-87;
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20

QY      10 SCFRLTECLSPSLTDB-----KVAY---LSLHPVLDL-----FVSESVAE 51
DB      68 SC-----SCFLQSPRRASSVPGTPTKTSASDFDRPLRPVIVDSEGTVSFLSDSKKE 122
QY      52 TVEKMLRKTNKAKDESPKESVYQDTNMGVVYELNSYLEQRLDTGDNHLLLEYLS 111
DB      123 QMPLTSPFDEBQDCSR-----LLELVKDISSHLDVTALCHKIPLHNG 168
QY      112 IIRATRADGFAFLFLSECNNSLCVFIRPGMKEGQPLIPAGPIYQGT----- 160
DB      169 LI-----SADRYSLPLVCEDSNDKFL-----SRLF---DYABGSTLEASNNCIRL 213
QY      161 -----ISAYVAKSRKTLVIEDIIGDERPRPGTGLSEGTRIQSVLCPIVTAIGDLIGILE 215
DB      214 EWNKGIYGVHAAFGEPILINKDAYEDPRFNAEVDQITGYKTSILCMPINKRREBVGVAAQ 273
QY      216 LY--RHNGKAFCLSHDEVATNLAAMASVAIHQVQCRLAKQTELDPLDVSKTYEDN 273
DB      274 AINKSGNGGTFTBEKEDPFAAYLAFCGIVLHNAQLVETSLLENKRQVLLDLASLIFE 333
QY      274 IVALDSLLEHMIYAKULVNADRCALFQVHDHKNELYSDLFDIGSEKGEPIFKTKIEIR 333
DB      334 QQSLEVLILKTIAAITISPMQYQCTIPIVDEDCDSFSBVHMECEBELKSSDTLTRERD 393
QY      334 FS--IEKGIAGQVARTGEVLNIPDAYADPRF---NREVDLYTGYTTRNLCMPIVS--RGS 387
DB      394 ANRNINWYAYQVKNKTMPLNIPDVSXKDRFMTNEMNGININQCCIRSLDCTPIKNKKNK 453
QY      388 VTGVQVNWKISGS-----APSKTDENNFKMFAVFCALALHCAMMYHRIIRSECTYRTM 442
DB      454 VTGVCQLVNKKKEETTGKVKAFENRNDQFLAEFAVIFCGSIGTONTMYEAVERAMAKQWYTL 513
QY      443 EKLSYHSICTSEEMOGMARFRLPRRI-----CRDLFPHFIQGPENMMPGFIYVMI 494
DB      514 EVLSYHNSAAEEETREIQ--SLAAAVPSPAOTLKITPDSFSEFELSDLETYLCITRMWT 571
QY      495 HRSCTGSCFLELEKCRFIMSVKKNYRR--VPYHNMKHAVTVAHCVAYLANN--NGLFTDL 551
DB      572 LNLVQNVQMKHEVLCCKWILSVKKNYKRVNAVHNMRRHFNTPAQCMFALYKAKKIQKRLD 631
QY      552 ERKGLLIACDHDHGRGFSNSYIQKFDHPLAALYSTSTMEQHNPSTQVSLQLEGNHIF 611
DB      632 EILALLILAAISHDDHGGVNNSYIQRESEHPLAQYCHSIMEHNFDCSLMILNSPGNOL 691
QY      612 STLSSEYEOVLLEIRKAIATADLAFGNRKQLEMYQTSGLYNHNSHNDRYVIGLMT 671
DB      692 SGSLSEYKTKTKIKQALITADTALYIKRGEEFELIMKNQVLEPDRHQCEPLAMIMT 751

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:55:36 ; Search time 116 Seconds  
(without alignments)  
2867.174 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206  
Sequence: 1 MEDGSPNNASCFRRUTECFL.....GPGAPSKSTPEKLVNVED 796

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:\*

- 1: /cgn2\_6/prodata/1/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4206	100.0	796	3	US-09-321-801-15 Sequence 15, Appl
2	4206	100.0	796	4	US-10-618-252-15 Sequence 15, Appl
3	4123	98.0	794	6	US-11-045-860-1 Sequence 1, Appl1
4	4080	97.0	779	6	US-11-045-860-3 Sequence 3, Appl1
5	3997	95.0	803	4	US-10-440-998-4 Sequence 4, Appl1
6	3993	94.9	789	3	US-09-321-801-2 Sequence 2, Appl1
7	3993	94.9	789	4	US-10-618-252-2 Sequence 2, Appl1
8	3951.5	93.9	773	4	US-10-202-107-2 Sequence 2, Appl1
9	3951.5	93.9	773	5	US-10-887-276-2 Sequence 2, Appl1
10	3878	92.2	779	3	US-09-420-190-1 Sequence 1, Appl1
11	3878	92.2	779	4	US-10-458-839-1 Sequence 1, Appl1
12	3878	92.2	779	4	US-10-440-998-6 Sequence 6, Appl1
13	3873	92.1	766	4	US-10-440-998-2 Sequence 2, Appl1
14	3867	91.9	791	3	US-09-321-801-4 Sequence 4, Appl1
15	3867	91.9	791	4	US-10-618-252-4 Sequence 4, Appl1
16	1795	42.7	362	6	US-11-045-860-2 Sequence 2, Appl1
17	1726	41.0	329	5	US-10-771-833-26 Sequence 26, Appl
18	1726	41.0	329	5	US-10-886-949-26 Sequence 26, Appl
19	1543	36.7	300	3	US-09-321-801-13 Sequence 13, Appl
20	1543	36.7	300	4	US-10-618-252-13 Sequence 13, Appl
21	1010	24.0	1284	4	US-10-256-144-5 Sequence 5, Appl1
22	1010	24.0	1284	6	US-11-097-143-42399 Sequence 42399, A
23	1010	24.0	1284	6	US-11-097-143-42399 Sequence 5, Appl1
24	967.5	23.0	934	4	US-10-168-402-39 Sequence 39, Appl
25	965.5	23.0	934	3	US-09-891-216-12 Sequence 12, Appl
26	965.5	23.0	934	3	US-09-891-216-15 Sequence 15, Appl
27	965.5	23.0	934	4	US-10-168-402-2 Sequence 2, Appl1

28	931.5	22.1	684	4	US-10-168-402-6 Sequence 6, Appl1
29	929	22.1	684	3	US-09-891-216-14 Sequence 14, Appl
30	929	22.1	684	4	US-10-168-402-4 Sequence 4, Appl1
31	929	22.1	684	4	US-10-746-197-1 Sequence 1, Appl1
32	924	22.0	833	3	US-09-891-216-3 Sequence 3, Appl1
33	918	21.8	875	4	US-10-115-515-10 Sequence 10, Appl
34	918	21.8	875	5	US-10-353-575A-10 Sequence 10, Appl
35	912.5	21.7	874	4	US-10-427-223-3 Sequence 3, Appl1
36	912.5	21.7	874	5	US-10-837-081-3 Sequence 3, Appl1
37	912.5	21.7	875	4	US-10-115-515-23 Sequence 23, Appl
38	912.5	21.7	875	4	US-10-094-168B-5 Sequence 5, Appl1
39	912.5	21.7	875	5	US-10-771-833-1 Sequence 1, Appl1
40	912.5	21.7	875	5	US-10-886-949-1 Sequence 1, Appl1
41	912.5	21.7	875	5	US-10-353-575A-23 Sequence 23, Appl
42	909	21.6	921	3	US-09-883-825-39 Sequence 39, Appl
43	909	21.6	921	4	US-10-094-989-5 Sequence 5, Appl1
44	909	21.6	921	4	US-10-697-894-39 Sequence 39, Appl
45	908	21.6	942	3	US-09-883-825-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-09-321-801-15  
Sequence 15, Application US/09321801  
Patent No. US20020115176A1  
GENERAL INFORMATION:  
APPLICANT: Lanfear, Jeremy  
APPLICANT: Robas, Nicola M.  
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
FILE REFERENCE: PC9477A  
CURRENT APPLICATION NUMBER: US/09/321,801  
EARLIER FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: 9826777.6  
EARLIER FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: 9823882.7  
EARLIER FILING DATE: 1998-10-30  
EARLIER APPLICATION NUMBER: 9811500.9  
EARLIER FILING DATE: 1998-05-28  
EARLIER APPLICATION NUMBER: 9808247.1  
EARLIER FILING DATE: 1998-04-09  
EARLIER APPLICATION NUMBER: 9910801.1  
EARLIER FILING DATE: 1999-05-10  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 796  
TYPE: PRT  
ORGANISM: Mouse  
US-09-321-801-15  
Query Match 100.0%; Score 4206; DB 3; Length 796;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEDGSPNNASCFRRUTECFLSPSLTDEKVAVYLSHPQVLEDFVSSVSATETKMLKRR	60
DB	1	MEDGSPNNASCFRRUTECFLSPSLTDEKVAVYLSHPQVLEDFVSSVSATETKMLKRR	60
QY	61	TNKAKEPSPKESRQODTMQGVYELNSYIQRDLDTGGDNLLLYELSSIRIRTKAD	120
DB	61	TNKAKEPSPKESRQODTMQGVYELNSYIQRDLDTGGDNLLLYELSSIRIRTKAD	120
QY	121	GFALYFAGECNNSLCYFIPGMEKEGPRLLIPAGPITGGTTISAYVAKSRKTLVVEDLIGD	180
DB	121	GFALYFAGECNNSLCYFIPGMEKEGPRLLIPAGPITGGTTISAYVAKSRKTLVVEDLIGD	180
QY	181	ERRPRGTGSGSGRIGSVLCPIVTAIGDILGILEYRHMKEAFCLSHOEVAITANLAWA	240
DB	181	ERRPRGTGSGSGRIGSVLCPIVTAIGDILGILEYRHMKEAFCLSHOEVAITANLAWA	240
QY	241	SVAIHQVQVRGLAKQTELDNDFLDVSKTYFDNIIVAIIDSLIHIMITYAKVLVNAIRCALF	300

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Db      241 SVAIHQVQCRGLAQOTELANDFLDVSCTYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Qy      301 QVDHKNKELYSDFDIEGKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIIPDAYADP 360
Db      301 QVDHKNKELYSDFDIEGKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIIPDAYADP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Qy      541 LQNNNGLFTDLERKGLIACLDHDFGFSNSYLQKFDHPLAALYSTIMEOHHSQTV 600
Db      541 LQNNNGLFTDLERKGLIACLDHDFGFSNSYLQKFDHPLAALYSTIMEOHHSQTV 600
Qy      601 SILQLEGNHIFSTLSSSEYEQVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Db      601 SILQLEGNHIFSTLSSSEYEQVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Qy      661 HDRVYIGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMDBRDKD 720
Db      661 HDRVYIGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMDBRDKD 720
Qy      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPPLKACRDLNOMEKVIRGETAMWISGPGP 780
Db      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPPLKACRDLNOMEKVIRGETAMWISGPGP 780
Qy      781 APSKSTPEKLVKVED 796
Db      781 APSKSTPEKLVKVED 796

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RESULT 2
US-10-618-252-15
; Sequence 15, Application US/10618252
; Publication No. US20040018542A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Kobas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477B
; CURRENT APPLICATION NUMBER: US/10/618,252
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: 9826777.6
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 9823882.7
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 9811500.9
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 9908247.1
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 9910801.1
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Mouse
US-10-618-252-15

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Query Match      100.0%; Score 4206; DB 4; Length 796;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEDGSPNNASCFRRLTTECFSLPSLTDEKVKAYLSLHPVLDEPNVSEBSVSAETVEKMLRK 60
Db      1 MEDGSPNNASCFRRLTTECFSLPSLTDEKVKAYLSLHPVLDEPNVSEBSVSAETVEKMLRK 60
Qy      61 TNKADBPSPKXVSRYQDTNMQGVYELNSYIEORLDTGCGNHLLYELSSIRATACD 120
Db      61 TNKADBPSPKXVSRYQDTNMQGVYELNSYIEORLDTGCGNHLLYELSSIRATACD 120
Qy      121 GPALYFLGECNNSLCVFIPGMKKGOPRLIPAGPTTQGTTSAYAVASRKTLVLDIGD 180
Db      121 GPALYFLGECNNSLCVFIPGMKKGOPRLIPAGPTTQGTTSAYAVASRKTLVLDIGD 180
Qy      181 ERFPRGTLESQTRIQSYLCLPIVTAIGDLIGILELYHMKKEAFCLSHQVATANLMA 240
Db      181 ERFPRGTLESQTRIQSYLCLPIVTAIGDLIGILELYHMKKEAFCLSHQVATANLMA 240
Qy      241 SVAIHQVQCRGLAQOTELANDFLDVSCTYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Db      241 SVAIHQVQCRGLAQOTELANDFLDVSCTYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Qy      301 QVDHKNKELYSDFDIEGKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIIPDAYADP 360
Db      301 QVDHKNKELYSDFDIEGKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIIPDAYADP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Qy      541 LQNNNGLFTDLERKGLIACLDHDFGFSNSYLQKFDHPLAALYSTIMEOHHSQTV 600
Db      541 LQNNNGLFTDLERKGLIACLDHDFGFSNSYLQKFDHPLAALYSTIMEOHHSQTV 600
Qy      601 SILQLEGNHIFSTLSSSEYEQVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Db      601 SILQLEGNHIFSTLSSSEYEQVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Qy      661 HDRVYIGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMDBRDKD 720
Db      661 HDRVYIGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKKLGIOPIPMDBRDKD 720
Qy      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPPLKACRDLNOMEKVIRGETAMWISGPGP 780
Db      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPPLKACRDLNOMEKVIRGETAMWISGPGP 780
Qy      781 APSKSTPEKLVKVED 796
Db      781 APSKSTPEKLVKVED 796

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RESULT 3
US-11-045-860-1
; Sequence 1, Application US/11045860
; Publication No. US20050202550A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; APPLICANT: Pandit, Jaywardan
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5' -CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
; FILE REFERENCE: PC25194A
; CURRENT APPLICATION NUMBER: US/11/045,860
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/552,761
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3

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SEQ ID NO 1  
LENGTH: 794  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-11-045-860-1

Query Match 98.0%; Score 4123; DB 6; Length 794;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

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QY 1 MEDGPNNSACRRRLTECFSLDEKRLKAYLSLHPQLDEFVSSVAETVEKMLKXK 60
DB 1 MEDGPNNSACRRRLTECFSLDEKRLKAYLSLHPQLDEFVSSVAETVEKMLKXK 60
QY 61 TNKADBPSPKESRYQDTNMGVVYELNSYIEORLDGTGDNDHLLYELSSIRIATKAD 120
DB 61 TNKADBPSPKESRYQDTNMGVVYELNSYIEORLDGTGDNDHLLYELSSIRIATKAD 120
QY 121 GVALYFLGSCNNSLCVFIIPGMEGQPLIPAGPIQTGTTISAVAKSKTLLVEDIIGD 180
DB 121 GVALYFLGSCNNSLCVFIIPGMEGQPLIPAGPIQTGTTISAVAKSKTLLVEDIIGD 180
QY 181 EEPREGTGESGRISQVCLPIVTAIGDLIGILEYRHMGEAFCLSHOEVAATNLMAWA 240
DB 181 EEPREGTGESGRISQVCLPIVTAIGDLIGILEYRHMGEAFCLSHOEVAATNLMAWA 240
QY 241 SVAIHQVQCRGLAKQTEINDPLLDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALF 300
DB 241 SVAIHQVQCRGLAKQTEINDPLLDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALF 300
QY 301 QVDHKKELYSDFDIEGEEKGPIFKTKTEIRFSIEKGIAGQAVATGEVLNIPDAVADP 360
DB 301 QVDHKKELYSDFDIEGEEKGPIFKTKTEIRFSIEKGIAGQAVATGEVLNIPDAVADP 360
QY 361 RFRREVDLTGYTTRNIIICMPIYSGSVIGVQMNKISGSAFSTKDENNFKMAFAFCAL 420
DB 361 RFRREVDLTGYTTRNIIICMPIYSGSVIGVQMNKISGSAFSTKDENNFKMAFAFCAL 420
QY 421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEWQGLMRPNLCRDIELPHFDIG 480
DB 421 ALHCANMYHRIHSECIYRVTMKLSYHSICTSEWQGLMRPNLCRDIELPHFDIG 480
QY 481 PFENMMPGIFVYMIHRSCTGSCFLEKLCRFINSVKKNRVRPYHNMKAATVAHGMAYAI 540
DB 481 PFENMMPGIFVYMIHRSCTGSCFLEKLCRFINSVKKNRVRPYHNMKAATVAHGMAYAI 540
QY 541 LQNNNGLFTELKRGILLIACLDHHRGSNSYLQKFDHPLAALYSTMEQHHSQTV 600
DB 541 LQNNNGLFTELKRGILLIACLDHHRGSNSYLQKFDHPLAALYSTMEQHHSQTV 600
QY 601 SIQLGEGNIFSTLSSEYEQVLEIRKAIITADLALYFGNRKQLEMYQTSILNHNOS 660
DB 601 SIQLGEGNIFSTLSSEYEQVLEIRKAIITADLALYFGNRKQLEMYQTSILNHNOS 660
QY 661 HRDRVIGLMMTACDLSVTKLMPVTKLTANDIYAEFAEGDEMKKLGIOPIPMMDRDKRD 720
DB 661 HRDRVIGLMMTACDLSVTKLMPVTKLTANDIYAEFAEGDEMKKLGIOPIPMMDRDKRD 720
QY 721 EYVQGGQGFNNAVAIPCYTTLTGQILPTEPRLKACPDNLNOMKEVIRGEETAMWISGPGP 780
DB 721 EYVQGGQGFNNAVAIPCYTTLTGQILPTEPRLKACPDNLNOMKEVIRGEETAMWISGPGP 780
QY 781 APSKSTPEKLNKVED 796
DB 779 ATSKSTSEKTRKVD 794

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## RESULT 4

US-11-045-860-3

Sequence 3, Application US/11045860

Publication No. US20050202550A1

GENERAL INFORMATION:

APPLICANT: Pfizer, Inc.

APPLICANT: Pandit, Jayvardan  
TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5' -CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
FILE REFERENCE: PC25194A  
CURRENT APPLICATION NUMBER: US/11/045,860  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 60/552,761  
PRIOR FILING DATE: 2004-03-12  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3  
LENGTH: 779  
TYPE: PRT  
ORGANISM: Mus musculus  
US-11-045-860-3

Query Match 97.0%; Score 4080; DB 6; Length 779;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 7 LTDEKAYALSLHPQYLDEFVSSVAETVEKMLKRTKADBPSPKESRYQDTNMVG 83
QY 84 VYELNSYIEORLDGTGDNDHLLYELSSIRIATKADGVALYFLGSCNNSLCVFIIPGK 143
DB 67 VYELNSYIEORLDGTGDNDHLLYELSSIRIATKADGVALYFLGSCNNSLCVFIIPGK 126
QY 144 EGQPLIPAGPIQTGTTISAVAKSKTLLVEDIIGDERFPRTGIESGTRIQSVCLPI 203
DB 127 EGQPLIPAGPIQTGTTISAVAKSKTLLVEDIIGDERFPRTGIESGTRIQSVCLPI 186
QY 204 VTAIGDLIGILEYRHMGEAFCLSHOEVAATNLMAWAIAHQVQCRGLAKQTEINDPL 263
DB 187 VTAIGDLIGILEYRHMGEAFCLSHOEVAATNLMAWAIAHQVQCRGLAKQTEINDPL 246
QY 264 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDIEGEEKG 323
DB 247 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDIEGEEKG 306
QY 324 PIFKTKTEIRFSIEKGIAGQAVATGEVLNIPDAVADPRENREVDLTGYTTRNIIICMPIY 383
DB 307 PIFKTKTEIRFSIEKGIAGQAVATGEVLNIPDAVADPRENREVDLTGYTTRNIIICMPIY 366
QY 384 SRGSVIGVQMNKISGSAFSTKDENNFKMAFAFCALALHCANMYHRIHSECIYRVME 443
DB 367 SRGSVIGVQMNKISGSAFSTKDENNFKMAFAFCALALHCANMYHRIHSECIYRVME 426
QY 444 KLSYHSICTSEWQGLMRPNLCRDIELPHFDIGPENMMPGIFVYMIHRSCTGSCF 503
DB 427 KLSYHSICTSEWQGLMRPNLCRDIELPHFDIGPENMMPGIFVYMIHRSCTGSCF 486
QY 504 ELEKLCRFINSVKKNRVRPYHNMKAATVAHGMAYAILQNNNGLFTELKRGILLIACLD 563
DB 487 ELEKLCRFINSVKKNRVRPYHNMKAATVAHGMAYAILQNNNGLFTELKRGILLIACLD 546
QY 564 DLDHRGFSNSYLQKFDHPLAALYSTMEQHHSQTVSILQLEGNHIFSTLSSEYEQVL 623
DB 547 DLDHRGFSNSYLQKFDHPLAALYSTMEQHHSQTVSILQLEGNHIFSTLSSEYEQVL 606
QY 624 EIRKAIITADLALYFGNRKQLEMYQTSILNHNOSHHRVIGLMMTACDLSVTKLMP 683
DB 607 EIRKAIITADLALYFGNRKQLEMYQTSILNHNOSHHRVIGLMMTACDLSVTKLMP 666
QY 684 VTKLTANDIYAEFAEGDEMKKLGIOPIPMMDRDKDEVPQGGQGFNNAVAIPCYTTLTG 743
DB 667 VTKLTANDIYAEFAEGDEMKKLGIOPIPMMDRDKDEVPQGGQGFNNAVAIPCYTTLTG 726
QY 744 ILPTEPRLKACPDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLNKVED 796
DB 727 ILPTEPRLKACPDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLNKVED 779

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RESULT 5  
 US-10-440-998-4  
 ; Sequence 4, Application US/10440998  
 ; Publication No. US20030215919A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loughney, Kate  
 ; TITLE OF INVENTION: Phosphodiesterase 8A  
 ; FILE REFERENCE: 27866/35047  
 ; CURRENT APPLICATION NUMBER: US/10/440,998  
 ; CURRENT FILING DATE: 2003-05-19  
 ; PRIOR APPLICATION NUMBER: US/09/686,055  
 ; PRIOR FILING DATE: 2000-10-11  
 ; PRIOR APPLICATION NUMBER: 08/951,648  
 ; PRIOR FILING DATE: 1997-10-16  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 803  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-440-998-4

Query Match 95.0%; Score 3997; DB 4; Length 803;  
 Best Local Similarity 95.4%; Pred. No. 0;  
 Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESVAETVEKMLRK 60  
 DB 15 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESVAETVEKMLRK 74  
 QY 61 TNKADSPSPKESVRDYDTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120  
 DB 75 NKSSEDESAPKESVRDYDTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 134  
 QY 121 GPALYFLGECNNSLCTFPPGKEGKPRLLIPAGPIQTGTTSAVYAKSKRTLLVEDILGD 180  
 DB 135 GPALYFLGECNNSLCTFPPGKEGKPRLLIPAGPIQTGTTSAVYAKSKRTLLVEDILGD 194  
 QY 181 BRFPFGTGESGTRIQSVLCLPIVTAIGDLIGLIELYRHMKEAFCLSHQEVATANILMA 240  
 DB 195 BRFPFGTGESGTRIQSVLCLPIVTAIGDLIGLIELYRHMKEAFCLSHQEVATANILMA 254  
 QY 241 SVAIHQOVQCRGLAKQTELANDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300  
 DB 255 SVAIHQOVQCRGLAKQTELANDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 314  
 QY 301 QVDHKNKEIYSDLPDIEGKEGKPIFKKTKETIRFSIEKGIAGQVARTGEVANIIDAADP 360  
 DB 315 QVDHKNKEIYSDLPDIEGKEGKPIFKKTKETIRFSIEKGIAGQVARTGEVANIIDAADP 374  
 QY 361 RNRREVDLYTGYTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSGKTDENNFMFAVFCAL 420  
 DB 375 RNRREVDLYTGYTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSGKTDENNFMFAVFCAL 434  
 QY 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARICRDIELFHPDIG 480  
 DB 435 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARICRDIELFHPDIG 494  
 QY 481 PRNNMPPGIFVTYMHRSCTSCPELEKLCRFITMSYKQNRVRYNNHKAIVTAHQMAY 540  
 DB 495 PRNNMPPGIFVTYMHRSCTSCPELEKLCRFITMSYKQNRVRYNNHKAIVTAHQMAY 554  
 QY 541 LONNNGLFTDLERKGLIACLDHGRGFSNSYQKPDHPLAALYSTSTMQHHFSQTV 600  
 DB 555 LONNNGLFTDLERKGLIACLDHGRGFSNSYQKPDHPLAALYSTSTMQHHFSQTV 614  
 QY 601 SILQEGHNIFSTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSILANQS 660  
 DB 615 SILQEGHNIFSTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSILANQS 674  
 QY 661 HRDRVIGLMTACDLCSVTKLMPVTKLTAANDIYAEFMAEGDEMKGLGIOPIMMDRDKD 720  
 DB 675 HRDRVIGLMTACDLCSVTKLMPVTKLTAANDIYAEFMAEGDEMKGLGIOPIMMDRDKD 734

QY 721 EVPOGQGFYNAVAIPCYTTLTQILPTEPILKACRDNLANQMEKVIIRGEETAMNISGPGP 780  
 DB 735 EVPOGQGFYNAVAIPCYTTLTQILPTEPILKACRDNLANQMEKVIIRGEETAMNISGPGP 794  
 QY 781 APSKSTPE 788  
 DB 795 AOKAASR 802

RESULT 6  
 US-09-321-801-2  
 ; Sequence 2, Application US/09321801  
 ; Patent No. US20020115176A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lanfear, Jeremy  
 ; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
 ; FILE REFERENCE: PC9477A  
 ; CURRENT APPLICATION NUMBER: US/09/321,801  
 ; CURRENT FILING DATE: 1999-05-27  
 ; EARLIER APPLICATION NUMBER: 9826777.6  
 ; EARLIER FILING DATE: 1998-12-04  
 ; EARLIER APPLICATION NUMBER: 9823882.7  
 ; EARLIER FILING DATE: 1998-10-30  
 ; EARLIER APPLICATION NUMBER: 9811500.9  
 ; EARLIER FILING DATE: 1998-05-28  
 ; EARLIER APPLICATION NUMBER: 9908247.1  
 ; EARLIER FILING DATE: 1998-04-09  
 ; EARLIER APPLICATION NUMBER: 9910801.1  
 ; EARLIER FILING DATE: 1999-05-10  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 789  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-321-801-2

Query Match 94.9%; Score 1993; DB 3; Length 789;  
 Best Local Similarity 95.3%; Pred. No. 0;  
 Matches 751; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESVAETVEKMLRK 60  
 DB 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESVAETVEKMLRK 60  
 QY 61 TNKADSPSPKESVRDYDTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120  
 DB 61 NKSSEDESAPKESVRDYDTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120  
 QY 121 GPALYFLGECNNSLCTFPPGKEGKPRLLIPAGPIQTGTTSAVYAKSKRTLLVEDILGD 180  
 DB 121 GPALYFLGECNNSLCTFPPGKEGKPRLLIPAGPIQTGTTSAVYAKSKRTLLVEDILGD 180  
 QY 181 BRFPFGTGESGTRIQSVLCLPIVTAIGDLIGLIELYRHMKEAFCLSHQEVATANILMA 240  
 DB 181 BRFPFGTGESGTRIQSVLCLPIVTAIGDLIGLIELYRHMKEAFCLSHQEVATANILMA 240  
 QY 241 SVAIHQOVQCRGLAKQTELANDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300  
 DB 241 SVAIHQOVQCRGLAKQTELANDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300  
 QY 301 QVDHKNKEIYSDLPDIEGKEGKPIFKKTKETIRFSIEKGIAGQVARTGEVANIIDAADP 360  
 DB 301 QVDHKNKEIYSDLPDIEGKEGKPIFKKTKETIRFSIEKGIAGQVARTGEVANIIDAADP 360  
 QY 361 RNRREVDLYTGYTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSGKTDENNFMFAVFCAL 420  
 DB 361 RNRREVDLYTGYTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSGKTDENNFMFAVFCAL 420  
 QY 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARICRDIELFHPDIG 480

Db 421 ALHCANMYHRIHSECIRYVMEKLSYHSICTSEEMOGLMOFTLVRUCKEITELFHPDIG 480  
QY 481 PERNMPGIFVYMIHRSOGTSCFELEKLCRFIMSVKKNYRVRPYNNMKAAVVAHCVMAI 540  
Db 481 PERNMPGIFVYMIHRSOGTSCFELEKLCRFIMSVKKNYRVRPYNNMKAAVVAHCVMAI 540  
QY 541 LONNNGLFTDLERKGLLIACLDHDLHGFNSYLOKFDHPLTALYSTMEQHHSQTV 600  
Db 541 LONNHTLFTDLERKGLLIACLDHDLHGFNSYLOKFDHPLTALYSTMEQHHSQTV 600  
QY 601 SILOEGHNIFFSTLSSEYEQVLEIRKAIITDIALYFGNKKOLEMYQTSILNHNOS 660  
Db 601 SILOEGHNIFFSTLSSEYEQVLEIRKAIITDIALYFGNKKOLEMYQTSILNHNOS 660  
QY 661 HHDRIYGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDBRDKD 720  
Db 661 HHDRIYGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDBRDKD 720  
QY 721 EYPOGOLGFYNAVAIPCTYTLTQIILPTEPLKACRDNINOMEKYIRGETAMWISGPGP 780  
Db 721 EYPOGOLGFYNAVAIPCTYTLTQIILPTEPLKACRDNINOMEKYIRGETAMWISGPGP 780  
QY 781 APSKSTPE 788  
Db 781 AOKAAASE 788  
RESULT 7  
US-10-618-252-2  
; Sequence 2, Application US/10618252  
; Publication No. US20040018542A1  
; GENERAL INFORMATION:  
; APPLICANT: Lanfear, Jeremy  
; APPLICANT: Robae, Nicola M.  
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES  
; FILE REFERENCE: PC9477B  
; CURRENT APPLICATION NUMBER: US/10/618,252  
; PRIOR FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: 9826777.6  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 9823882.7  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 9811500.9  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 9908247.1  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 9910801.1  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 2  
; LENGTH: 789  
; TYPE: PRT  
; ORGANISM: Human  
US-10-618-252-2  
Query Match 94.9%; Score 3993; DB 4; Length 789;  
Best Local Similarity 95.3%; Pred. No. 0;  
Matches 751; Conservative 19; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MEDGSPNNASCPRRLTECFSPSLTDEKVAAYLSLHPQVLDEFVSSESVAETVEKMLK 60  
Db 1 MEDGSPNNASCPRRLTECFSPSLTDEKVAAYLSLHPQVLDEFVSSESVAETVEKMLK 60  
QY 61 TNFAKDESPKESVRYQDTMVGQVYVELNSYIEQRDLDTGDNHLLLYELSSITRIATKAD 120  
Db 61 TNFAKDESPKESVRYQDTMVGQVYVELNSYIEQRDLDTGDNHLLLYELSSITRIATKAD 120  
QY 121 GFLALYTGECNNISLCVPIPGMKEGORPLIPAGITOGTTISAVVASKRTLLVEEDLGD 180  
Db 121 GFLALYTGECNNISLCVPIPGMKEGORPLIPAGITOGTTISAVVASKRTLLVEEDLGD 180  
QY 181 ERPRGTGLESRTIQSVLCLPIVTAIGDLIGILELYRHMGKFAFCLSHOEVAATANIAMA 240

Db 181 ERPRGTGLESRTIQSVLCLPIVTAIGDLIGILELYRHMGKFAFCLSHOEVAATANIAMA 240  
QY 241 SVALIHQVOCGGLAKQOTELNDFLDVSTYEDNIVAIDSLIEHIMIYAKONVNDRCALF 300  
Db 241 SVALIHQVOCGGLAKQOTELNDFLDVSTYEDNIVAIDSLIEHIMIYAKONVNDRCALF 300  
QY 301 QVDHKNKELSDLPDIGEKEGKPIFKTKTEIRFSEIKGIAQVARTGEVANIIPDAVDP 360  
Db 301 QVDHKNKELSDLPDIGEKEGKPIFKTKTEIRFSEIKGIAQVARTGEVANIIPDAVDP 360  
QY 361 RFRREVDLYTGYTTNLIICMPIVSRGSYIGVQVWNKISGSASFSTDDNNFQMAVFCAL 420  
Db 361 RFRREVDLYTGYTTNLIICMPIVSRGSYIGVQVWNKISGSASFSTDDNNFQMAVFCAL 420  
QY 421 ALHCANMYHRIHSECIRYVMEKLSYHSICTSEEMOGLMOPNIPARI CROITELFHPDIG 480  
Db 421 ALHCANMYHRIHSECIRYVMEKLSYHSICTSEEMOGLMOPNIPARI CROITELFHPDIG 480  
QY 481 PERNMPGIFVYMIHRSOGTSCFELEKLCRFIMSVKKNYRVRPYNNMKAAVVAHCVMAI 540  
Db 481 PERNMPGIFVYMIHRSOGTSCFELEKLCRFIMSVKKNYRVRPYNNMKAAVVAHCVMAI 540  
QY 541 LONNNGLFTDLERKGLLIACLDHDLHGFNSYLOKFDHPLTALYSTMEQHHSQTV 600  
Db 541 LONNHTLFTDLERKGLLIACLDHDLHGFNSYLOKFDHPLTALYSTMEQHHSQTV 600  
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Db 601 SILOEGHNIFFSTLSSEYEQVLEIRKAIITDIALYFGNKKOLEMYQTSILNHNOS 660  
QY 661 HHDRIYGLMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDBRDKD 720  
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QY 721 EYPOGOLGFYNAVAIPCTYTLTQIILPTEPLKACRDNINOMEKYIRGETAMWISGPGP 780  
Db 721 EYPOGOLGFYNAVAIPCTYTLTQIILPTEPLKACRDNINOMEKYIRGETAMWISGPGP 780  
QY 781 APSKSTPE 788  
Db 781 AOKAAASE 788  
RESULT 8  
US-10-202-107-2  
; Sequence 2, Application US/10202107  
; Publication No. US20030096323A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: James, Larry C.  
; APPLICANT: Lebel, Lorraine A.  
; APPLICANT: Menitzi, Frank S.  
; APPLICANT: Strick, Christine A.  
; TITLE OF INVENTION: PD810 CELL-BASED ASSAY AND SEQUENCES  
; FILE REFERENCE: PC23111ANIS  
; CURRENT APPLICATION NUMBER: US/10/202,107  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/308,978  
; PRIOR FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 773  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-202-107-2  
Query Match 93.9%; Score 3951.5; DB 4; Length 773;  
Best Local Similarity 97.9%; Pred. No. 0;  
Matches 757; Conservative 3; Mismatches 8; Indels 5; Gaps 4;  
QY 24 LIDKVKAYLSLHPQVLDEFVSSESVAETVEKMLKRTKTKAKDBSPKESVRYQDTMVG 83

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Db 4 LTDEKVAVLSLHPQVLDSESVSAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQG 62
QY 84 VVYELNSYIEQRLDPTGDNHLLLYELSSIRIATADGFALYFLGECNNSLCVFIPGMK 143
Db 63 VVYELNSYIEQRLDPTGDNHLLLYELSSIRIATADGFALYFLGECNNSLCVFIPGMK 122
QY 144 EGQPLIPAGPITQGTTSAYAVAKSRKTLVEDILGDERPFRGTGLESSTRIQSVLCPI 203
Db 123 EGQPLIPAGPITQGTTSAYAVAKSRKTLVEDILGDERPFRGTGLESSTRIQSVLCPI 182
QY 204 VTAIGDLIGILELYRHMGKEAFCLSHQEVATNLAMASVALIHQOVCGRLAKQTEINDFL 263
Db 183 VTAIGDLIGILELYRHMGKEAFCLSHQEVATNLAMASVALIHQOVCGRLAKQTEINDFL 242
QY 264 LDVSKTYPDNIYALDLSLEHIMIYAKNLVNAORCALFOVDHKNKELYSGLFDIGEEKGK 323
Db 243 LDVSKTYPDNIYALDLSLEHIMIYAKNLVNAORCALFOVDHKNKELYSGLFDIGEEKGK 302
QY 324 PIFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAVADPRFNEBVDLYGTYTRNIIICMPIV 383
Db 303 PIFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAVADPRFNEBVDLYGTYTRNIIICMPIV 362
QY 384 SRGSYIGVQVWVKISGSAFSKTDENNFMFAVFCALALHCANMYHRIHSECIYRTME 443
Db 421 SRGSYIGVQV-WVKISGSAFSKTDENNFMFAVFCALALHCANMYHRIHSECIYRTME 421
QY 444 KLSYHSICTSEBMOGLMFPNLPARICRDIELFHFDIGFENMMPGIFVYMIHRSCTSCF 503
Db 422 KLSYHSICTSEBMOGLMFPNLPARICRDIELFHFDIGFENMMPGIFVYMIHRSCTSCF 481
QY 504 ELEKLCRFIMSVKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 563
Db 482 ELEKLCRFIMSVKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 541
QY 564 DLDHGFNSYLOKRDHPLAALYSTMEQHHFSQTVSIIQLEGHNIFFSTLSSSEYQVL 623
Db 542 DLDHGFNSYLOKRDHPLAALYSTMEQHHFSQTVSIIQLEGHNIFFSTLSS-YESVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEEMVQTSGLNLHNSHRDVIYGLMTRACDLCSTYKLM 683
Db 601 EIIRKAIATDIALYFGNRKQLEEMVQTSGLNLHNSHRDVIYGLMTRACDLCSTYKLM 660
QY 684 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDRKDEVPQQLGFYNAVALPCYTTLLQ 743
Db 661 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDRKDEVPQQLGFYNAVALPCYTTLLQ 720
QY 744 ILPTEPLLKACRDNLQMEKYIRGEETAMWISGPGAPSKSTPEKLVKVED 796
Db 721 ILPTEPLLKACRDNLQMEKYIRGEETAMWIS--GPATSKSTSEKPRKVD 771

RESULT 9
US-10-887-276-2
; Sequence 2, Application US/10887276
; Publication No. US20050026236A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: James, Larry C.
; APPLICANT: Leibel, Lorraine A.
; APPLICANT: Menniti, Frank S.
; APPLICANT: Strick, Christine A.
; TITLE OF INVENTION: PDE10 CELL-BASED ASSAY AND SEQUENCES
; FILE REFERENCE: PC23111ANIS
; CURRENT APPLICATION NUMBER: US/10/887,276
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US/10/202,107
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/308,978
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
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; LENGTH: 773
; TYPE: prt
; ORGANISM: Rattus sp.
US-10-887-276-2

Query Match          93.9%; Score 3951.5; DB 5; Length 773;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 757; Conservative 3; Mismatches 8; Indels 5; Gaps 4;

QY 24 LTDEKVAVLSLHPQVLDSESVSAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQG 83
Db 4 LTDEKVAVLSLHPQVLDSESVSAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQG 62
QY 84 VVYELNSYIEQRLDPTGDNHLLLYELSSIRIATADGFALYFLGECNNSLCVFIPGMK 143
Db 63 VVYELNSYIEQRLDPTGDNHLLLYELSSIRIATADGFALYFLGECNNSLCVFIPGMK 122
QY 144 EGQPLIPAGPITQGTTSAYAVAKSRKTLVEDILGDERPFRGTGLESSTRIQSVLCPI 203
Db 123 EGQPLIPAGPITQGTTSAYAVAKSRKTLVEDILGDERPFRGTGLESSTRIQSVLCPI 182
QY 204 VTAIGDLIGILELYRHMGKEAFCLSHQEVATNLAMASVALIHQOVCGRLAKQTEINDFL 263
Db 183 VTAIGDLIGILELYRHMGKEAFCLSHQEVATNLAMASVALIHQOVCGRLAKQTEINDFL 242
QY 264 LDVSKTYPDNIYALDLSLEHIMIYAKNLVNAORCALFOVDHKNKELYSGLFDIGEEKGK 323
Db 243 LDVSKTYPDNIYALDLSLEHIMIYAKNLVNAORCALFOVDHKNKELYSGLFDIGEEKGK 302
QY 324 PIFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAVADPRFNEBVDLYGTYTRNIIICMPIV 383
Db 303 PIFKKTKEIRFSIEKGIAGQVARTGEVLNIPDAVADPRFNEBVDLYGTYTRNIIICMPIV 362
QY 384 SRGSYIGVQVWVKISGSAFSKTDENNFMFAVFCALALHCANMYHRIHSECIYRTME 443
Db 421 SRGSYIGVQV-WVKISGSAFSKTDENNFMFAVFCALALHCANMYHRIHSECIYRTME 421
QY 444 KLSYHSICTSEBMOGLMFPNLPARICRDIELFHFDIGFENMMPGIFVYMIHRSCTSCF 503
Db 422 KLSYHSICTSEBMOGLMFPNLPARICRDIELFHFDIGFENMMPGIFVYMIHRSCTSCF 481
QY 504 ELEKLCRFIMSVKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 563
Db 482 ELEKLCRFIMSVKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 541
QY 564 DLDHGFNSYLOKRDHPLAALYSTMEQHHFSQTVSIIQLEGHNIFFSTLSSSEYQVL 623
Db 542 DLDHGFNSYLOKRDHPLAALYSTMEQHHFSQTVSIIQLEGHNIFFSTLSS-YESVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEEMVQTSGLNLHNSHRDVIYGLMTRACDLCSTYKLM 683
Db 601 EIIRKAIATDIALYFGNRKQLEEMVQTSGLNLHNSHRDVIYGLMTRACDLCSTYKLM 660
QY 684 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDRKDEVPQQLGFYNAVALPCYTTLLQ 743
Db 661 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDRKDEVPQQLGFYNAVALPCYTTLLQ 720
QY 744 ILPTEPLLKACRDNLQMEKYIRGEETAMWISGPGAPSKSTPEKLVKVED 796
Db 721 ILPTEPLLKACRDNLQMEKYIRGEETAMWIS--GPATSKSTSEKPRKVD 771

RESULT 10
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
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; CURRENT APPLICATION NUMBER: US/09/420,190  
; CURRENT FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FaSTSeq for Windows Version 3.0  
; SEQ ID NO: 1  
; LENGTH: 779  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-420-190-1

Query Match 92.2%; Score 3878; DB 3; Length 779;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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24 LTDEKVKAYLSLHPQVLDFEVSSEVSAETVEKMLKRTNKAKDEBSPKESVRYODTNMG 83
14 LTDEKVKAYLSLHPQVLDFEVSSEVSAETVEKMLKRNKKSDEBSPKESVRYODTNMG 73
84 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFPFGMK 143
74 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFPFGIK 133
144 EGQPLIPAGPTTGGTTSAYVAKSRKTLVEDIIGDERPPRGTSLESGTRIQSVLCPI 203
134 EGQPLIPAGPTTGGTTSAYVAKSRKTLVEDIIGDERPPRGTSLESGTRIQSVLCPI 193
204 VTAIGDLIGILELYRMGKEAFCLSHQEVATANLAWASVAIHQOVCRGLAQTEINDEL 263
194 VTAIGDLIGILELYRMGKEAFCLSHQEVATANLAWASVAIHQOVCRGLAQTEINDEL 253
264 LDVSKTYFPDNIYAIDSLLEHIMIYAKNLVADRCLFQVDHKNKELYSDFDIGEEKGK 323
254 LDVSKTYFPDNIYAIDSLLEHIMIYAKNLVADRCLFQVDHKNKELYSDFDIGEEKGK 313
324 PI FPKTKETIRFSEIKGIAGVARTGEVLNI PDAYADPRFNREVDLYGTGTTNII LCMPIV 383
314 PVFKTKETIRFSEIKGIAGVARTGEVLNI PDAYADPRFNREVDLYGTGTTNII LCMPIV 373
384 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALHCANMYRIRHSECIYVTWE 443
374 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALHCANMYRIRHSECIYVTWE 433
444 KLSYHSICTSEEMQGLMRFNLPARICRDIELFHDIGPEENMFGIFVYMIHRSCTSGCF 503
434 KLSYHSICTSEEMQGLMRFNLPARICRDIELFHDIGPEENMFGIFVYMIHRSCTSGCF 493
504 ELEKLCRFPTMSYKKNRYRVPYHNWKAAVYVAHCVTAIILONNHTLFTDLERKGLLIACLG 563
494 ELEKLCRFPTMSYKKNRYRVPYHNWKAAVYVAHCVTAIILONNHTLFTDLERKGLLIACLG 553
564 DLDHRGFSNSYLQKFDHPPLAALYSTSTMEQHHSQTVSIIQLGEGHNI FSTLSSSEYQVL 623
554 DLDHRGFSNSYLQKFDHPPLAALYSTSTMEQHHSQTVSIIQLGEGHNI FSTLSSSEYQVL 613
624 EIRIKAIITDIALYFNGRKQLEEMYTQTSILNINSHRDVYGLMWTACDLCSTVKLMP 683
614 EIRIKAIITDIALYFNGRKQLEEMYTQTSILNINSHRDVYGLMWTACDLCSTVKLMP 673
684 VTKLTANDIYAEFWAGDEMKKLGIOPI PMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 743
674 VTKLTANDIYAEFWAGDEMKKLGIOPI PMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 733
744 ILPTEPLKACRDNI LQMEKVI RGETATWISSPSVAQKAAASE 788
734 ILPTEPLKACRDNI LQMEKVI RGETATWISSPSVAQKAAASE 778
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RESULT 11  
US-10-458-839-1  
; Sequence 1, Application US/10458839  
; Publication No. US20030215898A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Hunter, John Joseph  
; APPLICANT: Williamson, Mark  
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic  
; TITLE OF INVENTION: Nucleotide Phosphodiesterase  
; FILE REFERENCE: 5800-71  
; CURRENT APPLICATION NUMBER: US/10/458,839  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FaSTSeq for Windows Version 3.0  
; SEQ ID NO: 1  
; LENGTH: 779  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-458-839-1

Query Match 92.2%; Score 3878; DB 4; Length 779;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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24 LTDEKVKAYLSLHPQVLDFEVSSEVSAETVEKMLKRTNKAKDEBSPKESVRYODTNMG 83
14 LTDEKVKAYLSLHPQVLDFEVSSEVSAETVEKMLKRNKKSDEBSPKESVRYODTNMG 73
84 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFPFGMK 143
74 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVFPFGIK 133
144 EGQPLIPAGPTTGGTTSAYVAKSRKTLVEDIIGDERPPRGTSLESGTRIQSVLCPI 203
134 EGQPLIPAGPTTGGTTSAYVAKSRKTLVEDIIGDERPPRGTSLESGTRIQSVLCPI 193
204 VTAIGDLIGILELYRMGKEAFCLSHQEVATANLAWASVAIHQOVCRGLAQTEINDEL 263
194 VTAIGDLIGILELYRMGKEAFCLSHQEVATANLAWASVAIHQOVCRGLAQTEINDEL 253
264 LDVSKTYFPDNIYAIDSLLEHIMIYAKNLVADRCLFQVDHKNKELYSDFDIGEEKGK 323
254 LDVSKTYFPDNIYAIDSLLEHIMIYAKNLVADRCLFQVDHKNKELYSDFDIGEEKGK 313
324 PI FPKTKETIRFSEIKGIAGVARTGEVLNI PDAYADPRFNREVDLYGTGTTNII LCMPIV 383
314 PVFKTKETIRFSEIKGIAGVARTGEVLNI PDAYADPRFNREVDLYGTGTTNII LCMPIV 373
384 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALHCANMYRIRHSECIYVTWE 443
374 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALHCANMYRIRHSECIYVTWE 433
444 KLSYHSICTSEEMQGLMRFNLPARICRDIELFHDIGPEENMFGIFVYMIHRSCTSGCF 503
434 KLSYHSICTSEEMQGLMRFNLPARICRDIELFHDIGPEENMFGIFVYMIHRSCTSGCF 493
504 ELEKLCRFPTMSYKKNRYRVPYHNWKAAVYVAHCVTAIILONNHTLFTDLERKGLLIACLG 563
494 ELEKLCRFPTMSYKKNRYRVPYHNWKAAVYVAHCVTAIILONNHTLFTDLERKGLLIACLG 553
564 DLDHRGFSNSYLQKFDHPPLAALYSTSTMEQHHSQTVSIIQLGEGHNI FSTLSSSEYQVL 623
554 DLDHRGFSNSYLQKFDHPPLAALYSTSTMEQHHSQTVSIIQLGEGHNI FSTLSSSEYQVL 613
624 EIRIKAIITDIALYFNGRKQLEEMYTQTSILNINSHRDVYGLMWTACDLCSTVKLMP 683
614 EIRIKAIITDIALYFNGRKQLEEMYTQTSILNINSHRDVYGLMWTACDLCSTVKLMP 673
684 VTKLTANDIYAEFWAGDEMKKLGIOPI PMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 743
674 VTKLTANDIYAEFWAGDEMKKLGIOPI PMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 733
744 ILPTEPLKACRDNI LQMEKVI RGETATWISSPSVAQKAAASE 788
734 ILPTEPLKACRDNI LQMEKVI RGETATWISSPSVAQKAAASE 778
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RESULT 12
US-10-440-998-6
; Sequence 6, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-998-6

Query Match          92.2%; Score 3878; DB 4; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

24 LTDEKVKAYLSLHPQVLDLDFVSESVSAETVEKMLKRTKNKADSPSPKVSRYODTNNG 83
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14 LTDEKVKAYLSLHPQVLDLDFVSESVSAETVEKMLKRTKNKADSPSPKVSRYODTNNG 73
|||||
84 VVTEINSLYIBORLDTGDNHLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGK 143
|||||
74 VVTEINSLYIBORLDTGDNHLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGK 133
|||||
144 EGQPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPPRGGLBEGSTRIOSVLCPI 203
|||||
134 EGKPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPPRGGLBEGSTRIOSVLCPI 193
|||||
204 VTAIGDLIGILELYRHMGKEAFCLSHOEVAITANLAMASVAIHQOVQCRGLAKOTELNDFL 263
|||||
194 VTAIGDLIGILELYRHMGKEAFCLSHOEVAITANLAMASVAIHQOVQCRGLAKOTELNDFL 253
|||||
264 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNDRCALFOVDHKNKELYSDFDIGEKEGK 323
|||||
254 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNDRCALFOVDHKNKELYSDFDIGEKEGK 313
|||||
324 PIFKTKETIRFSIEKIGAGVARTGEVLANIPDAVADPRFNREVDLYTGYTTNIIICMPIV 383
|||||
314 PVEFKTKETIRFSIEKIGAGVARTGEVLANIPDAVADPRFNREVDLYTGYTTNIIICMPIV 373
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384 SRGSIVGVQVQVNNKISGSAFSTKTDENNFKMFPAVFCALALHCANNYHRIHSECIYRTME 443
|||||
374 SRGSIVGVQVQVNNKISGSAFSTKTDENNFKMFPAVFCALALHCANNYHRIHSECIYRTME 433
|||||
444 KLSYHSICTSESEMOGLMRFNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQSGTSCF 503
|||||
434 KLSYHSICTSESEMOGLMRFNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQSGTSCF 493
|||||
504 ELEKLCRFIMSVKKNYRRVRYNNHMGAVTVAHCMYALIONNHGJFTDLERKGLIACLC 563
|||||
494 ELEKLCRFIMSVKKNYRRVRYNNHMGAVTVAHCMYALIONNHGJFTDLERKGLIACLC 553
|||||
564 DLDHRGFSNSYLQKFDHPLAALYSTSTWEOHNFQSVTSILOLEGHNIPSTLSSSEYEOVL 623
|||||
554 DLDHRGFSNSYLQKFDHPLAALYSTSTWEOHNFQSVTSILOLEGHNIPSTLSSSEYEOVL 613
|||||
624 EIRKAAIATDLALYKGRKQLEEMVQGSILNHNOSHDRVYIGLMMTPACDLCSTYKCLMP 683
|||||
614 EIRKAAIATDLALYKGRKQLEEMVQGSILNHNOSHDRVYIGLMMTPACDLCSTYKCLMP 673
|||||
684 VTKLTANDIYAEFNAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 743
|||||
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Db          674 VTKLTANDIYAEFNAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLLQ 733
Qy          744 ILPTEBPLKACRDNLINOMKEVIRGEETAMWISGPGAPSKSTPE 788
Db          734 ILPTEBPLKACRDNLINOMKEVIRGEETAMWISGPGAPSKSTPE 778

RESULT 13
US-10-440-998-2
; Sequence 2, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc. feature
; LOCATION: (290)
; OTHER INFORMATION: The amino acid is either Pro or Leu
US-10-440-998-2

Query Match          92.1%; Score 3873; DB 4; Length 766;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

24 LTDEKVKAYLSLHPQVLDLDFVSESVSAETVEKMLKRTKNKADSPSPKVSRYODTNNG 83
|||||
1 LTDEKVKAYLSLHPQVLDLDFVSESVSAETVEKMLKRTKNKADSPSPKVSRYODTNNG 60
|||||
84 VVTEINSLYIBORLDTGDNHLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGK 143
|||||
61 VVTEINSLYIBORLDTGDNHLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGK 120
|||||
144 EGQPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPPRGGLBEGSTRIOSVLCPI 203
|||||
121 EGKPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPPRGGLBEGSTRIOSVLCPI 180
|||||
204 VTAIGDLIGILELYRHMGKEAFCLSHOEVAITANLAMASVAIHQOVQCRGLAKOTELNDFL 263
|||||
181 VTAIGDLIGILELYRHMGKEAFCLSHOEVAITANLAMASVAIHQOVQCRGLAKOTELNDFL 240
|||||
264 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNDRCALFOVDHKNKELYSDFDIGEKEGK 323
|||||
241 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNDRCALFOVDHKNKELYSDFDIGEKEGK 300
|||||
324 PIFKTKETIRFSIEKIGAGVARTGEVLANIPDAVADPRFNREVDLYTGYTTNIIICMPIV 383
|||||
301 PVEFKTKETIRFSIEKIGAGVARTGEVLANIPDAVADPRFNREVDLYTGYTTNIIICMPIV 360
|||||
384 SRGSIVGVQVQVNNKISGSAFSTKTDENNFKMFPAVFCALALHCANNYHRIHSECIYRTME 443
|||||
361 SRGSIVGVQVQVNNKISGSAFSTKTDENNFKMFPAVFCALALHCANNYHRIHSECIYRTME 420
|||||
444 KLSYHSICTSESEMOGLMRFNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQSGTSCF 503
|||||
421 KLSYHSICTSESEMOGLMRFNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQSGTSCF 480
|||||
504 ELEKLCRFIMSVKKNYRRVRYNNHMGAVTVAHCMYALIONNHGJFTDLERKGLIACLC 563
|||||
481 ELEKLCRFIMSVKKNYRRVRYNNHMGAVTVAHCMYALIONNHGJFTDLERKGLIACLC 540
|||||
564 DLDHRGFSNSYLQKFDHPLAALYSTSTWEOHNFQSVTSILOLEGHNIPSTLSSSEYEOVL 623
|||||
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Db	541	DLDRGFNSYQKFDHPILAAALYSTSTYEHQHPISQTVASITLQEGHNIPSTLSSSEYQVL	600
Qy	624	ELIRKAIATATLALVFGRNKKOLEEYMQYGSLLAHNQSHDRYVIGLMTTACDLCSTYKLMF	683
Db	601	ELIRKAIATATDALVFGRNKKOLEEYMQYGSLLAHNQSHDRYVIGLMTTACDLCSTYKLMF	660
Qy	684	VTKLTANDIYAEFMAEGDEMKLGIQIPIPMORDRDKDEVPOGQLGFYNAVAIPCYTTLNQ	743
Db	661	VTKLTANDIYAEFMAEGDEMKLGIQIPIPMORDRDKDEVPOGQLGFYNAVAIPCYTTLNQ	720
Qy	744	ILPPTPELTKACRDNIHQEKVIRGEETAMWISGPGAPASKSTPE	788
Db	721	ILPPTPELTKACRDNIHQEKVIRGEETITWISSPEVAQKAAASE	765

	RESULT 14	
US-09-321-801-4	Sequence 4, Application US/09321801	
	Patent No. US20020115176A1	
	GENERAL INFORMATION:	
	APPLICANT: Lanfear, Jeremy	
	APPLICANT: Robas, Nicola M.	
	TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES	
	FILE REFERENCE: PC9477A	
	CURRENT APPLICATION NUMBER: US/09/321,801	
	CURRENT FILING DATE: 1999-05-27	
	EARLIER APPLICATION NUMBER: 9826777.6	
	EARLIER FILING DATE: 1998-12-04	
	EARLIER APPLICATION NUMBER: 9823882.7	
	EARLIER FILING DATE: 1998-10-30	
	EARLIER APPLICATION NUMBER: 9811500.9	
	EARLIER FILING DATE: 1998-05-28	
	EARLIER APPLICATION NUMBER: 9906247.1	
	EARLIER FILING DATE: 1998-04-09	
	EARLIER APPLICATION NUMBER: 9910801.1	
	EARLIER FILING DATE: 1999-05-10	
	NUMBER OF SEQ ID NOS: 19	
	SOFTWARE: PatentIn Ver. 2.1	
	SEQ ID NO 4	
	LENGTH: 791	
	TYPE: PRT	
	ORGANISM: Human	
US-09-321-801-4		
Query Match	91.9% Score 3867; DB 3; Length 791;	
Best Local Similarity	95.2%; Pred. No. 0;	
Matches 728; Conservative	19; Mismatches 16; Indels 0; Gaps 0,	
DQ	24 LTDEKVAAYLSIAHPVLDFEVSYSAEVTEKMLRKTNKADKPSPKVSRYQDTNQG	83
DB	26 LTDEKVAAYLSIAHPVLDFEVSYSAEVTEKMLRKKNKSSEDSAPKEVSRYYQDTNQG	85
DY	84 VVYLENSTIEQLDLDGNDGNHLLLYELSSITRATKADGPALYEFGCNNSLCVPFIPGMK	143
DB	86 VVYLENSTIEQLDLDGNDGNQLLYELSSITKATRADGFALYFEGCNSSLCIFPPIGIK	145
DY	144 EGQPRLLIAGPITGGTTISAVYAASRKTLLVEDILGDERFPFRGTLESGTRIQSVLCPI	203
DB	146 ECKPRLLIAGPITGGTTISAVYAASRKTLLVEDILGDERFPFRGTLESGTRIQSVLCPI	205
DY	204 VTALIGDLIGILELYHHMGKEAFCLSHQVATAKNLMAASAHLINOVOCRGIAKOTELNFL	263
DB	206 VTALIDLLIGILELYHHMGKEAFCLSHQEVATKNLMAASALHNQOVCRGLAQETELNFL	265
DY	264 LDVSKTYEPDNIVAIISLSLEHIMIYAKNLVNADRCLFQVDHKKELYSDLPDIGEEKGK	323
DB	266 LDVSKTYEPNNIVAIISLSLEHIMIYAKNLVNADRCLLFQVDHKKELYSDLPDIGEEKGK	325
DY	324 PIPEKTKTEIRFSIEKGIAQGVARTGEVLANIPRAVADPRNRREVDLYTGVTNTNIICMPIV	383
DB	326 PIPEKTKTEIRFSIEKGIAQGVARTGEVLANIPRAVADPRNRREVDLYTGVTNTNIICMPIV	385

QY	384	SRGSVIGVQWVNKISGASFKSTDENNKMAVFCALLHCKANMYHRIHSHCIYRVME	443
Db	386	SRGSVIGVQWVNKISGASFKSTDENNKMAVFCALLHCKANMYHRIHSHCIYRVME	445
QY	444	KLVSYSICTSEEMOGIMFNLPARICRDIELPHFDIGPENNMPCGIVVMYHRSCTGSCF	503
Db	446	KLVSYSICTSEEMOGIMFNLPARICRDIELPHFDIGPENNMPCGIVVMYHRSCTGSCF	505
QY	504	ELEKLCREIMSVKKNYRRVPYHNMKHAYVAHCMAIILONNNGLTDLERKGLIACLC	563
Db	506	ELEKLCREIMSVKKNYRRVPYHNMKHAYVAHCMAIILONNNGLTDLERKGLIACLC	565
QY	564	DLDRGFENSTYQKRDHPALALYSTSTBOHFSQTSVILQEGHNIPTSLSSBEYQYL	623
Db	566	DLDRGFENSTYQKRDHPALALYSTSTBOHFSQTSVILQEGHNIPTSLSSBEYQYL	625
QY	624	ELIRKAIATLALYFGNRRKOLEEMYOTGSLINLHNOHSHRDVYIGLMTACDLCSTVKLMP	683
Db	626	ELIRKAIATLALYFGNRRKOLEEMYOTGSLINLHNOHSHRDVYIGLMTACDLCSTVKPMP	685
QY	684	VTKLTANDIYAEFWAEGDBMKKLGIOTIPMDNRDKDEVIPQQLGFTYNAVALPCYTTLQ	743
Db	686	VTKLTANDIYAEFWAEGDBMKKLGIOTIPMDNRDKDEVIPQQLGFTYNAVALPCYTTLQ	745
QY	744	ILPPTPEPLKACRONLQNMEXKIRBBETAMTISGCPAPASCTPE	788
Db	746	ILPPTPEPLKACRONLQNMEXKIRBBETAMTISGCPAPASCTPE	790

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RESULT 15
US-10-618-252-4
/ Sequence 4, Application US/10618252
/ Publication No. US20040018542n1
/ GENERAL INFORMATION:
/ APPLICANT: Lanfear, Jeremy
/ APPLICANT: Robas, Nicola M.
/ TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
/ FILE REFERENCE: PC9477B
/ CURRENT APPLICATION NUMBER: US-10/618,252
/ CURRENT FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: 9826777.6
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 9823882.7
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 9811500.9
/ PRIOR FILING DATE: 1998-05-28
/ PRIOR APPLICATION NUMBER: 9908247.1
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: 9910801.1
/ PRIOR FILING DATE: 1999-05-10
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 4
/ LENGTH: 791
/ TYPE: PRT
/ ORGANISM: Human
US-10-618-252-4

Query Match          91.9%; Score 3867; DB 4; Length 791;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 728; Conservative 19; Mismatches 18; Indels 0; Gaps 0.

QY      24  LTDEYKAYLSLHPVLDPEFSESATVEKWLKRKNKADESPKESRYODTNNG 83
DB      26  LTDEKVKYLSLHPVLDPEFSESATVEKWLKRKNKSEDESAPEKSRQDTNNG 85
QY      84  VVEENKSYIEORLDDGDNHLLVLESLIIRIATKADGFALYFLGCNNSLCVPIPGMK 143
DB      86  VVEENKSYIEORLDDGDNHLLVLESLIIRIATKADGFALYFLGCNNSLCIFPPGK 145
QY      144 EGCPRLIPAGPI TGCTTTSAVYAKSRKTLVEDILIGDRFPFGTLESGTRIQSVLCPI 203
DB      146 EGCPRLIPAGPI TGCTTTSAVYAKSRKTLVEDILIGDRFPFGTLESGTRIQSVLCPI 205

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OY 595 HPSQVTSILOEGHNIFSTLSSEYEQVLEIRKAIATDIALYFGNKKOLEMYQT--- 651
Db 233 HIAVGFKLQENECNCFQNLTKKQOSLRKQVIDLVLATDMSKHNLLADLKTWVETKKV 292
OY 652 ---GSLINHNOSHRDVRIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKKLG 708
Db 293 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTDRIWEEFROGDRERERG 352
OY 709 QIPIMDDKDEVPQOGLGFYNNAVAIPCYYTLTQIL-PPTPEPLKACRDNLNQMEKYR 767
Db 353 BISPWCDDKRNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADODILDLEDRNEWYQSTIP 411
OY 768 GEETAMWISGPGAPASKSTPEK 789
Db 412 -----QSPSPAP--DDPEE 423

RESULT 2
US-11-091-018-9
; Sequence 9, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretearedotcfr, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT FILING DATE: 2005-03-25
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-9

Query Match 7.5%; Score 315.5; DB 7; Length 585;
Best Local Similarity 25.4%; Pred. No. 1e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

OY 442 MEKLSYHSICTSEEWQGLMRFLPAR-----ICRDIELFHPDIGPEENMMPGIFVYMIHRS 497
Db 143 VKKLHSSSLTN---SSTPRFGVKTQEDVLAKEL-----DV---NKM-GHAFRIAMEL 190
OY 498 CG-----TSCFELEKCRFIWSVKKNYRR-VPHNMKHAVTVAHCM 537
Db 191 SGNRPFLVIMHTIFQERDLTKTFKIPVDLTLYLMTLEBDHYADVAYANNHIAADVOST 250
OY 538 YAILQNN--NGFLPTDLERKGLLIACLDLDRHGFNSYLOKFDHPPLAALYS-TSTMEOH 594
Db 251 HVLSTPLAEVFTDLEILAAIFASAIHDVDPGVSNQFLINTNSLALMTYNDSSVLENH 310
OY 595 HPSQVTSILOEGHNIFSTLSSEYEQVLEIRKAIATDIALYFGNKKOLEMYQT--- 651
Db 311 HIAVGFKLQENECNCFQNLTKKQOSLRKQVIDLVLATDMSKHNLLADLKTWVETKKV 370
OY 652 ---GSLINHNOSHRDVRIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKKLG 708
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Db 371 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTDRIWEEFROGDRERERG 430
OY 709 QIPIMDDKDEVPQOGLGFYNNAVAIPCYYTLTQIL-PPTPEPLKACRDNLNQMEKYR 767
Db 431 BISPWCDDKRNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADODILDLEDRNEWYQSTIP 489
OY 768 GEETAMWISGPGAPASKSTPEK 789
Db 490 -----QSPSPAP--DDPEE 501

RESULT 3
US-11-091-018-6
; Sequence 6, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretearedotcfr, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT FILING DATE: 2005-03-25
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-6

Query Match 7.5%; Score 315.5; DB 7; Length 673;
Best Local Similarity 25.4%; Pred. No. 1.3e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

OY 442 MEKLSYHSICTSEEWQGLMRFLPAR-----ICRDIELFHPDIGPEENMMPGIFVYMIHRS 497
Db 231 VKKLHSSSLTN---SSTPRFGVKTQEDVLAKEL-----DV---NKM-GHAFRIAMEL 278
OY 498 CG-----TSCFELEKCRFIWSVKKNYRR-VPHNMKHAVTVAHCM 537
Db 279 SGNRPFLVIMHTIFQERDLTKTFKIPVDLTLYLMTLEBDHYADVAYANNHIAADVOST 338
OY 538 YAILQNN--NGFLPTDLERKGLLIACLDLDRHGFNSYLOKFDHPPLAALYS-TSTMEOH 594
Db 339 HVLSTPLAEVFTDLEILAAIFASAIHDVDPGVSNQFLINTNSLALMTYNDSSVLENH 398
OY 595 HPSQVTSILOEGHNIFSTLSSEYEQVLEIRKAIATDIALYFGNKKOLEMYQT--- 651
Db 399 HIAVGFKLQENECNCFQNLTKKQOSLRKQVIDLVLATDMSKHNLLADLKTWVETKKV 458
OY 652 ---GSLINHNOSHRDVRIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKKLG 708
Db 459 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTDRIWEEFROGDRERERG 518
OY 709 QIPIMDDKDEVPQOGLGFYNNAVAIPCYYTLTQIL-PPTPEPLKACRDNLNQMEKYR 767
Db 519 BISPWCDDKRNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADODILDLEDRNEWYQSTIP 577
OY 768 GEETAMWISGPGAPASKSTPEK 789
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; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 12
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-12

Query Match      7.5%; Score 315.5; DB 6; Length 748;
Best Local Similarity 25.4%; Pred. No. 1.5e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWQGLMRNLPAR---ICRDIELFHFDIGPENMMPGIFVYMIHRS 497
DB 306 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVRRIAEI 353
QY 498 CG-----TSCPELEKLCRFINSVKKNYR--VPYNNMKAAVTVAHCM 537
DB 354 SGNRPITYIMHTIFQERDLTKFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 413
QY 538 YAILQNN--NGLFTDLERKGLLIACLDHLDHGRFSNSYLQFDPHPLAALYS-TSTMEOH 594
DB 414 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTSEBLAMVNDSSVLENH 473
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEBNYQT--- 651
DB 594 BISPCDGNNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDNREWYOSTIP 652
QY 709 QPIPMDDKDEBVGQGLGFYNAVAIPCYTTLTQIL-PTPEPLKACRDINQMEKVIYR 767
DB 594 BISPCDGNNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDNREWYOSTIP 652
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 653 -----QSPSPAP--DDPER 664

RESULT 7
US-10-492-835-28
; Sequence 28, Application US/10492835
; Publication No. US2005028960A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492,835
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 28
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-28

Query Match      7.5%; Score 315.5; DB 6; Length 748;
Best Local Similarity 25.4%; Pred. No. 1.5e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWQGLMRNLPAR---ICRDIELFHFDIGPENMMPGIFVYMIHRS 497
DB 306 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVRRIAEI 353
QY 498 CG-----TSCPELEKLCRFINSVKKNYR--VPYNNMKAAVTVAHCM 537
DB 354 SGNRPITYIMHTIFQERDLTKFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 413
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QY 538 YAILQNN--NGLFTDLERKGLLIACLDHLDHGRFSNSYLQFDPHPLAALYS-TSTMEOH 594
DB 414 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTSEBLAMVNDSSVLENH 473
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEBNYQT--- 651
DB 474 HLAVGFKLQENCDIFONLTQKOROSLRKAVIDIIVALTQWSKMNLLADLKTWETKCV 533
QY 652 ---GSLNHNSHNRDVIGLMWTACDLCSTYKLMVPVTKLTANDIYAEFPAEGDEMKKLG 708
DB 534 TSSGVLLDNTSDRIQVQNNVHCADLSNPTKPLQLYRQWTDRIWBEFFRQGDREBERGM 593
QY 709 QPIPMDDKDEBVGQGLGFYNAVAIPCYTTLTQIL-PTPEPLKACRDINQMEKVIYR 767
DB 594 BISPCDGNNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDNREWYOSTIP 652
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 653 -----QSPSPAP--DDPER 664

RESULT 8
US-11-091-018-2
; Sequence 2, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Grefarodotlr, Solveig
; APPLICANT: Thorleifsson, Gudmar
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091.018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-2

Query Match      7.5%; Score 315.5; DB 7; Length 809;
Best Local Similarity 25.4%; Pred. No. 1.7e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWQGLMRNLPAR---ICRDIELFHFDIGPENMMPGIFVYMIHRS 497
DB 367 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVRRIAEI 414
QY 498 CG-----TSCPELEKLCRFINSVKKNYR--VPYNNMKAAVTVAHCM 537
DB 415 SGNRPITYIMHTIFQERDLTKFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 474
QY 538 YAILQNN--NGLFTDLERKGLLIACLDHLDHGRFSNSYLQFDPHPLAALYS-TSTMEOH 594
DB 475 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTSEBLAMVNDSSVLENH 534
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEBNYQT--- 651
DB 535 HLAVGFKLQENCDIFONLTQKOROSLRKAVIDIIVALTQWSKMNLLADLKTWETKCV 594
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Db      354  SGNRP LTVIMHTIFQERDLTKTFKIPVDFTLITLMTLEBDYHADVAHYNNHIAADVOST 413
Qy      538  YAILONN--NGFLPTLERGGLIACCHDLDHGRFNSVLOKFDHLLALYS--TSMEOH 594
Db      414  HVLTLTPALFAVFTDEILAAIFASAIHVDHPGVSNOFLINTNELAMYNDSVLENH 473
Qy      595  HFSQTVSILQLEGHNFSTLSSSEYEQVLEIRKAIATDLALFQGNRKQLEMYOT--- 651
Db      474  HIAVGFKLQENECDFQULTKKQROSLAKMAIDVLATDMGKHMLLADLKTMYETKYV 533
Qy      652  ---GSLINHSGHRDVRIGLMTACDLCSVTKLMPVTKLTANDIYAEFAEDEMCKLGI 708
Db      534  TSSGVLTLIDNYSDRIQVLOQNMVHCADLSNPTKPLQLYRQWTDRIWEEFPGQDREERGM 593
Qy      709  QPIPMMDRKREBVGQGLGFYNAVAIPCYTLTQTL--PTEPBLKACDNLNOMEKVIR 767
Db      594  EISPMCDKRNA--SVEKSOVGFIYVHPLEMTWADLVHPDADDLDTLEDEMEYOSTIP 652
Qy      768  GSETAMWISGPGAP 782
Db      653  -----QSPSPAP 659

RESULT 12
US-10-873-528-12
; Sequence 12, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent In Ver. 2.1
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-12

Query Match      2.5%; Score 107; DB 6; Length 1216;
Best Local Similarity 18.9%; Pred. No. 0.33;
Matches 166; Conservative 119; Mismatches 273; Indels 320; Gaps 46;

Qy      46  ESVAETVEKMLKRTKTKAKD-----PSPKX-----VSRYODTN 80
Db      366  QSFMSDFEAYARQKQENAFEFADISHYTIILENFQVRSYGERFHEVAVDEODTN 425
Qy      81  MGVVYELNSYIEORLDTGSDNHLLEYLSIIRIATKADGAFALYLGECNSLGVFP 140
Db      426  -----HIQER-----MLELLS-----NGNRRPMVGDIKOSIYRF-- 454
Qy      141  GMEGQPRILPAGPIGTGTTISAVYAKSRKTLVLEDILDERPPGTGLSGSTRLOSVC 200
Db      455  --RQADPOIF-----NEKFOR-----YQNPQE----- 475
Qy      201  LPIVTAIGDLIGILELYRMGKEAPCLSHQEVATANTLMAVAIAHQVYCRGLAQTEIN 260
Db      476  -----GRLLILKENFR-----SSSEVLST-----NDVF 499
Qy      261  DFLLD--VSKYFDNIVALDISLLEHIMTYA--KNLVNADRCALLFOVDHKNKELYSDDLPI 316
Db      500  ERLMDQVEGEIINYDN-----KHQLVFANTKLTLPNPDKAAF-----LTYDKDDT 543

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Qy      317  GEEKGKPIFKKTYEIRFSI-----EKGI-----GOVARTGEVINTPDAVADP 360
Db      544  GEEBSQYETLGTGEMRLVIEIKLKHQEKVAFREIATLSSSRNDQILLALSEYGP 603
Qy      361  -----RPNREVDLYGTYYTRNLCPIVSRGSGVGVOMNKISGSAFSKTDENNFK 412
Db      604  VKTDGEQNNTYLSLEVQVWMLDTLRVIHNPLODYALV-----ALMKSPPMGFDEDELA 655
Qy      413  MFAVPCALAHCAAMMYHIRSE-----CIYRVTEKL--SVHSICTSEMOGLMR-- 461
Db      666  RLISQKADKQKHEMLYELCVNAQKASQKGLHTLALAEKUKQFNDILAS--WRIYAKTH 713
Qy      462  --FNLPARICHDILEFHD--IGPENMMPGIFVYMIHRSCTSGPE--LEKLCRFIMSV 515
Db      714  SLYDIWKIYND--RFYDYVYDALPN--GPANQANLYALALADQPEKSNFGLSFIIMI 770
Qy      516  KKNTRRVEYHNWKI--AVTYAHCMYAILONNGLFTDLEKGL--LIAQLCHDLD-- 566
Db      771  DQVLEA-----QHDLASVAVAPPRDAV-----ELMTIHKSQGLEFPYVFIANDDQFNK 819
Qy      567  -----HRGFSNYLQPDHPPLAALYSTSMEOHFSQTV--SILOEGHNIPST 613
Db      820  QDSMSEVILSRONGGVKTYANME-----TGAVED--HYPKTIKLSIPSLTYRQNEE 870
Qy      614  LSSSEYEQVLEIRKAIATDLALYF--GNRKQLEB--MYQTGSIN--LHNSHR 662
Db      871  LQLASYSQOMRLVYVAMTRAKKLYLVGKSRKELSEKVEYPAANGKLNSTVLOANRFQ 930
Qy      663  DRVIGLMMTACDLCSTVKLMPVTKLTAND--IYAEFAE-----GDEMKGLGIPT 711
Db      931  D-----WLMWISKVFTFKDKLNFYSYRFGEDQLTREAIQLELTSPLQDS 974
Qy      712  PMMDRDKREBVGQ-----OLGFYN-----AVAIPCYTLTQILPTEPBLKACDNLNQ 761
Db      975  SQADNRQSDITKELMLEMKVEYVNTLHRAHIELPSVQTSPLKQFYEPVMD----- 1026
Qy      762  WEKYRGEETAMWISGPGA-----PSKSTPEKX 790
Db      1027  -----MEGYE-----IAGQGSVGGKISPLDPFSIKENV 1056

RESULT 13
US-11-046-346-1
; Sequence 1, Application US/11046346
; Publication No. US20050255502A1
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Institute
; APPLICANT: D'Andrea, Alan D
; TITLE OF INVENTION: Method for Determination and Quantification of Radiation or Genotoxicity
; FILE REFERENCE: 7032/2082
; CURRENT APPLICATION NUMBER: US/11/046,346
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/540380
; PRIOR FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-346-1

Query Match      2.5%; Score 106; DB 7; Length 1451;
Best Local Similarity 18.0%; Pred. No. 0.53;
Matches 159; Conservative 131; Mismatches 266; Indels 326; Gaps 44;

Qy      21  SPSLTDEKVAUYLSLHPQVDEPFVSESATVEKMLKRTKTKAKDPSPKESVRYODTN 80
Db      592  SPSLTQE--RANLS-----DEQCTQVTS-----LLQVHSC--SQSQSPQASALYTD-- 633
Qy      81  MGVVYELNSYIEORLDTGSDNHLLEYLSIIRIATKADGAFALYLGECNSLGVFI 138

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Db 792 DI 793

RESULT 15  
US-10-821-234-1097  
; Sequence 1097, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmail, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 1097  
; LENGTH: 1094  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1097

Query Match 2.2%; Score 92.5; DB 6; Length 1094;

Best Local Similarity 17.7%; Pred. No. 5.8; Matches 128; Conservative 95; Mismatches 218; Indels 281; Gaps 33;

Qy 284 IMIYAKNLVNADRCALFYVDHKNKELYSN-----LPDICEKEKGP-----I 325  
Db 162 LRVNGRNLLSVN-----FDRTTTEKITYDHRKFLRLAIADTSGHPTLMPSKLMANVT 217  
Qy 326 FKTYKEIRFSIKGIAGQ-VARTGEVLNIPDAVADPRF-----NREYD 367  
Db 218 YSSTQIQA-SIQGTSEKVDYDGGGRIVSRVAFADGKTWSYTLKSMVLLHSORQYIF 276  
Qy 368 LYTGTTNIIICMPTVSRGVS-----IGVQGVN-NKISGSASFSTD--ENNFKMAVPCA 419  
Db 277 EYDMMDRLSALTMPSPVARTHTQITRSIGYRNINYPSPSNASITTDYNEGLLQTAFLG 336  
Qy 420 LALHCANNMYR-IRHSECIYRVTEKLSYHS-----ICT----- 452  
Db 337 TSNRVLFKRRQTRLSSEILYDSTRVSFTYDETAGVLKTVNLQSDGFCITIRYRQIGPLID 396  
Qy 453 -----SEEWQGLMRFN-----LPAICRDIELFHPD----- 478  
Db 397 RQIFRFSSEGMVNAHFDYSYDNSFRVTSMQGVINETPLP-----IDLYQFDDISGKVEQ 450  
Qy 479 IGFENMMPGIRVVMHNSCGTSCFELK-----LCRFIM----- 513  
Db 451 FGKF-----GVLYIDINQIISTAVMTYTHGFAHGRIKEIQYEIRPSLSLWYITIQDNGK 505  
Qy 514 -SVKQYRRVRYHN-----WKHAVVAHCWYAILQNNGLF 548  
Db 506 RVTKEIKIGPRANTTKAYEYDVQGLQTVVLEKIMRMYVDLNGNLHLNPSNSARL 565  
Qy 549 T-----DLERKGLLIACLCHDLDRGFSN-----SYLQKFD 579  
Db 566 TPLRYDLRDRITRLDGVRLDEDFLRQGTETFEYSSKGLLTRVYSSKSGMTVIYRYD 625  
Qy 580 HPLALYSTSTMEQH-----HFSQVSLT--QLEGHNFSTLSSE 618  
Db 626 GIGRRVSSKTSISGQHLQFFYADLTYPTRITTHVYNNHSSSEITSLYYDLQHLFAMEISSGD 685  
Qy 619 YEQVLEIRKAIITND-----LATYGNRKQLEMYQTSMLHNSQHRD--RVIGLMMT 671  
Db 686 -----EFTYASDNTCTPLAVSSNGMLAKQIQTAYGEIYFDSNIDPQLVIGFHGG 736  
Qy 672 ACDDCSVTKLMPVTKL-----TANDIYAEFWAEGD--EKKKLGIOPIPMMDRDKRDEVPO 724  
Db 737 LYD-----PLTFKLHGERDYDILAGRMTTPIEIKWRIKGDPAFENLYMFRANNPA 788

Qy 725 GOL-----GPNVAIPCYTT-----LTQILPPTPEPLKACRDNLNQWE 763  
Db 789 SKIHVYKQYITDVNSKMLVTFGPHLHNAIFGFPVPRKFDLIE---PSYELVKS-----QQWD 840  
Qy 764 KV 765  
Db 841 DI 842

Search completed: January 10, 2006, 14:07:17  
Job time : 31 secs